

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 16:57:42 / Search time 186 Seconds

(without alignments)
944.901 Million cell updates/sec

Title: US-10-618-570-2

Perfect score: 2059
Sequence: 1 MAQMDPDPDQEDTDSCTES.....DWKATRGVINFTRLTQKE 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_21:*

- 1: geneeqp19808:*
- 2: geneeqp19908:*
- 3: geneeqp20008:*
- 4: geneeqp20018:*
- 5: geneeqp20028:*
- 6: geneeqp20038:*
- 7: geneeqp20048:*
- 8: geneeqp20058:*
- 9: geneeqp20068:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2059	100.0	400	2	AAV03098 Bovine sc
2	1381	67.1	349	2	AAV05508 Scavenger
3	1381	67.1	453	2	AAV05509 Scavenger
4	1381	67.1	453	2	AAV27036 Bovine so
5	1047.5	50.9	451	2	AAV19708 Macrophag
6	1046.5	50.8	451	2	AD162129 Human mac
7	1042.5	50.6	358	2	AAV21513 Human sca
8	1042.5	50.6	358	2	AAV40803 Human sca
9	1042.5	50.6	358	2	AAV08078 Type II m
10	1042.5	50.6	358	4	AAV49716 Human typ
11	1042.5	50.6	358	7	ADB89003 Human mac
12	1042.5	50.6	358	7	ADQ39735 Human myo
13	1042.5	50.6	358	8	ADQ39731 Human myo
14	1042.5	50.6	358	8	ADQ39734 Human myo
15	1042.5	50.6	358	8	ADQ39733 Human myo
16	1042.5	50.6	451	2	AAV21512 Human sca
17	1042.5	50.6	451	2	AAV40802 Human sca
18	1042.5	50.6	451	2	AAV08077 Type I ma
19	1042.5	50.6	451	3	AAV08080 Protein o
20	1042.5	50.6	451	4	AAV49715 Human typ
21	1042.5	50.6	451	8	AD162127 Human mac
22	1042.5	50.6	451	8	AD162123 Human mac
23	1042.5	50.6	451	8	AD162125 Human mac
24	1042.5	50.6	451	8	AD162126 Human mac

25	1042.5	50.6	451	8	AD162124 Human mac
26	1042.5	50.6	451	8	AD114197 Novel hum
27	1042.5	50.6	451	8	ADQ39732 Human myo
28	1042.5	50.6	451	8	ADV45547 Homologue
29	1042.5	50.6	487	8	ADP24729 PRO polyP
30	1040.5	50.5	451	8	AD162128 Human mac
31	1039.5	50.5	451	8	AD162130 Human mac
32	1034.5	50.2	451	8	AD162131 Human mac
33	1032.5	50.1	451	8	AAV27035 Human sol
34	801	38.9	454	7	ADP28571 Murine ma
35	801	38.9	458	8	ADP45554 Mouse typ
36	680.5	33.1	502	8	ADP97493 CD1d-IgC
37	678.5	33.0	581	9	AAV28082 Circulari
38	678	32.9	128	9	ADV78149 Chicken I
39	678	32.9	152	2	AAV29307 Wild-type
40	678	32.9	152	2	AAV17867 Chicken a
41	678	32.9	152	8	ADP26980 Chicken a
42	678	32.9	152	8	AAV28059 Chicken a
43	678	32.9	153	9	AAV78159 Barley am
44	678	32.9	161	3	AAV44699 Potato pr
45	678	32.9	269	8	ADP97489 CD1d-IgC

ALIGNMENTS

RESULT 1
AAV03098
ID AAV03098 standard; protein; 400 AA.

AC AAV03098;
XX
XX
DT 03-DEC-1999 (first entry)
XX
XX
DE Bovine scavenger receptor class A (SCR)/avidin fusion protein.
XX
XX Scavenger receptor class A; SCR; avidin; fusion protein; bovine; ECD;
KW membrane-spanning domain; extracellular domain; biotin-binding activity;
KM endocytosis.
XX
XX Synthetic.
OS Bos taurus.
XX
XX WO9942577-A2.
XX
XX
PD 26-AUG-1999.
XX
XX
XX 23-FEB-1999; 99WO-GB000546.
XX
XX
XX 23-FEB-1998; 98GB-00003757.
PR 24-JUN-1998; 98GB-00013653.
XX
XX (EURO-) EUROGENE LTD.
XX
XX Y1a-Herttua1a S, Kulomaa M, Lehtolainen P, Marjomaki V, Airene K;
DR MPI: 1999-561345/47.
DR N-PSDB; AA09997.
XX
XX New fusion proteins having an extracellular domain with biotin-binding
PT activity, used to target biotinylated molecules to specific sites in
PT tissues.
XX
XX Claim 5: Page 21-23; 23pp; English.
XX
XX This invention describes a novel protein (A) which comprises a membrane-
XX spanning domain and an extracellular domain (ECD), where the ECD
XX comprises biotin-binding activity. Using the proteins or encoding nucleic
XX acid molecules it is possible to target biotinylated molecules to
XX specific sites in tissues. Molecules targeted in this way may be taken up
XX by the tissues or cells by endocytosis, allowing the molecules to exert
XX their effects within or on the cell. This sequence represents a bovine
XX scavenger receptor class A/avidin fusion protein which is used in the

CC description of the invention
XX
SQ Sequence 400 AA;
Query Match 100.0%; Score 2059; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.2e-156;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQMDPDDQEDBDTSCTESYKFPDARSVTALLPPIPKNGPTLQEMKSYKTALLITLYLIV 60
DB 1 MAQMDPDDQEDBDTSCTESYKFPDARSVTALLPPIPKNGPTLQEMKSYKTALLITLYLIV 60
QY 61 FVLVPIIIGIYAAQLKMKETKCTVGSVNADISPSPEKGSGSEDEMFRFAVMERMSNM 120
DB 61 FVLVPIIIGIYAAQLKMKETKCTVGSVNADISPSPEKGSGSEDEMFRFAVMERMSNM 120
QY 121 ESRIOYLSDBNEANLLDANKFONFSITTDQRFNDVLFQNSLLSSIQEHENIIGDISKSLV 180
DB 121 ESRIOYLSDBNEANLLDANKFONFSITTDQRFNDVLFQNSLLSSIQEHENIIGDISKSLV 180
QY 181 GLNTTVLDLPISITLNGRVQENAFKQOEEMRKLEERYNNAEIKSLDEKQVYLEQIK 240
DB 181 GLNTTVLDLPISITLNGRVQENAFKQOEEMRKLEERYNNAEIKSLDEKQVYLEQIK 240
QY 241 GEMKLNNTITNDLRKWEHSQTLKNITLLQGARCSLTGKWTNDLGSNMTIGAVNSRGE 300
DB 241 GEMKLNNTITNDLRKWEHSQTLKNITLLQGARCSLTGKWTNDLGSNMTIGAVNSRGE 300
QY 301 FTGYITLVATSNKESPLHGTONITNKRTQPTFGFTVWVKSEBSTTVFTGQCFIDRN 360
DB 301 FTGYITLVATSNKESPLHGTONITNKRTQPTFGFTVWVKSEBSTTVFTGQCFIDRN 360
QY 361 GKEVLKTMMLRSSVNDIGDMKATRVGINIFTRLRTOKE 400
DB 361 GKEVLKTMMLRSSVNDIGDMKATRVGINIFTRLRTOKE 400
RESULT 2
AAR05508
ID AAR05508 standard; protein; 349 AA.
XX
AC AAR05508;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 23-OCT-1990 (first entry)
XX
DE Scavenger receptor protein with affinity for acylated low density
lipoprotein (aLDL).
XX
KW Acylated low density lipoprotein; aLDL; atherosclerotic plaque; ds.
XX
OS Synthetic.
XX
PN WO9005748-A.
XX
PD 31-MAY-1990.
XX
PE 15-NOV-1988; 88US-00272002.
XX
PR 15-NOV-1988; 88US-00272002.
PR 09-AUG-1989; 89US-00391486.
AX
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Kodama T, Krieger M;
XX
DR WPI; 1990-193408/25.
DR N-PSDB; AAQ04925.
XX
PT New receptor protein - has affinity for acetylated low density
lipoprotein and corresponding antibodies and DNA sequences.
XX

PS Disclosure; Page ?; 79pp; English.
XX
CC Receptor protein, and fragments and analogues thereof may be immobilised
CC on a support and used in assay and purification of the aLDL target.
CC Labelled Abs, raised to the protein may be injected into the vascular
CC system to detect the presence of atherosclerotic plaques. (Updated on 31-
CC OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR
CC field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-
CC 2003 to correct PI field.)
XX
SQ Sequence 349 AA;
Query Match 67.1%; Score 1381; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 3e-102;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQMDPDDQEDBDTSCTESYKFPDARSVTALLPPIPKNGPTLQEMKSYKTALLITLYLIV 60
DB 1 MAQMDPDDQEDBDTSCTESYKFPDARSVTALLPPIPKNGPTLQEMKSYKTALLITLYLIV 60
QY 61 FVLVPIIIGIYAAQLKMKETKCTVGSVNADISPSPEKGSGSEDEMFRFAVMERMSNM 120
DB 61 FVLVPIIIGIYAAQLKMKETKCTVGSVNADISPSPEKGSGSEDEMFRFAVMERMSNM 120
QY 121 ESRIOYLSDBNEANLLDANKFONFSITTDQRFNDVLFQNSLLSSIQEHENIIGDISKSLV 180
DB 121 ESRIOYLSDBNEANLLDANKFONFSITTDQRFNDVLFQNSLLSSIQEHENIIGDISKSLV 180
QY 181 GLNTTVLDLPISITLNGRVQENAFKQOEEMRKLEERYNNAEIKSLDEKQVYLEQIK 240
DB 181 GLNTTVLDLPISITLNGRVQENAFKQOEEMRKLEERYNNAEIKSLDEKQVYLEQIK 240
QY 241 GEMKLNNTITNDLRKWEHSQTLKNITLLQ 272
DB 241 GEMKLNNTITNDLRKWEHSQTLKNITLLQ 272
RESULT 3
AAR05509
ID AAR05509 standard; protein; 453 AA.
XX
AC AAR05509;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 23-OCT-1990 (first entry)
XX
DE Scavenger receptor protein with affinity for acylated low density
lipoprotein (aLDL).
XX
KW Acylated low density lipoprotein; aLDL; atherosclerotic plaque; ds.
XX
OS Synthetic.
XX
PN WO9005748-A.
XX
PD 31-MAY-1990.
XX
PE 15-NOV-1988; 88US-00272002.
XX
PR 15-NOV-1988; 88US-00272002.
PR 09-AUG-1989; 89US-00391486.
AX
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Kodama T, Krieger M;
XX
DR WPI; 1990-193408/25.
DR N-PSDB; AAQ04925.
XX
PT New receptor protein - has affinity for acetylated low density
lipoprotein and corresponding antibodies and DNA sequences.
XX

PS Disclosure: Page 7; 79pp; English.

XX Receptor protein, and fragments and analogues thereof may be immobilised
CC on a support and used in assay and purification of the aLDL target.
CC Labelled Abs, raised to the protein may be injected into the vascular
CC system to detect the presence of atherosclerotic plaques. (Updated on 31-
CC OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR
CC field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-
CC 2003 to correct FI field.)

XX Sequence 453 AA;

Query Match 67.1%; Score 1381; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 4.3e-102;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWDPDQOEDTDSCTESVVFDPARSVTALLPPHPKNGPTLQEBMKSYKTLITLYLIV 60
DB 1 MAQWDPDQOEDTDSCTESVVFDPARSVTALLPPHPKNGPTLQEBMKSYKTLITLYLIV 60
QY 61 FVVLVPIIIGIYVAOQLKWKETKCTGVSVNADISPSPEKGNGSEDEMRPREAVMERMSNM 120
DB 61 FVVLVPIIIGIYVAOQLKWKETKCTGVSVNADISPSPEKGNGSEDEMRPREAVMERMSNM 120
QY 121 ESRIOYLSDNENANLDAKNFQNSITTDORFNDVLFQNSLLSSIOEHENIIGDISKSLIV 180
DB 121 ESRIOYLSDNENANLDAKNFQNSITTDORFNDVLFQNSLLSSIOEHENIIGDISKSLIV 180
QY 181 GIANTVLDLQFSIETLNGRVQENAFKQOEEMKLEERIYNASAEIKSLDEKQVLYEOEIK 240
DB 181 GIANTVLDLQFSIETLNGRVQENAFKQOEEMKLEERIYNASAEIKSLDEKQVLYEOEIK 240
QY 241 GEMKLNITNDRLKDMHESQTLKNITLLOG 272
DB 241 GEMKLNITNDRLKDMHESQTLKNITLLOG 272

RESULT 4
AAR27036
ID AAR27036 standard; protein; 453 AA.

XX AAR27036;
AC 23-SEP-2004 (revised)
DT 25-MAR-2003 (revised)
DT 20-MAY-1998 (first entry)

DE Bovine sol. scavenger receptor.

KM Macrophage; endotoxaemia; radiolabelled; toxic; degenerate.

XX Bos taurus.
OS Unidentified.

XX Key Location/Qualifiers
FT Domain 1..50 "cytoplasmic"
FT Domain 51..76 /note="transmembrane"
FT Domain 77..109 /note="spacer"
FT Domain 110..271 /note="alpha helical coiled coil"
FT Domain 272..343 /note="collagen binding"
FT Domain 341..451 /note="Cys-rich"

XX W09214482-A1.
XX 03-SEP-1992.
XX 21-FEB-1992; 92WO-US001370.

XX 22-FEB-1991; 91US-00662227.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Krieger M;

XX MPI: 1992-315935/38.

XX N-PSDB; AAQ28540.

XX Treatment and diagnosis of endotoxaemia and related disease states -
PT using a polypeptide fragment of the extracellular portion of a macrophage
PT scavenger receptor protein.

PS Disclosure: Page 38; 56pp; English.

XX The bovine scavenger receptor protein sequence was deduced from the DNA
CC sequence obtd. by screening a bovine lung cDNA library with degenerate
CC probes designed based on fragments of the purified scavenger receptor
CC protein. The scavenger receptor protein has a binding capacity for
CC acetylated low density lipoprotein (LDL) and binds endotoxin. Fragments
CC of the extracellular portion of the scavenger receptor protein inactivate
CC endotoxin-related substances and are used in the diagnosis and treatment
CC of endotoxaemia. They may be administered to patients at high risk of
CC symptomatic or endotoxic shock. The fragments may also be fixed to inert
CC supports for purification purposes. The fragments may be modified to have
CC greater binding affinity for the endotoxin-related substance than the
CC native scavenger receptor protein, or to more effectively neutralise the
CC toxic or pathogenic effects of moles. that bind the scavenger receptor
CC protein or of organisms which express such moles. See also AAR27035.
CC (Updated on 25-MAR-2003 to correct PN field.)

CC Revised record issued on 23-SEP-2004 : Correction to Feature Table Key

XX Sequence 453 AA;

Query Match 67.1%; Score 1381; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 4.3e-102;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWDPDQOEDTDSCTESVVFDPARSVTALLPPHPKNGPTLQEBMKSYKTLITLYLIV 60
DB 1 MAQWDPDQOEDTDSCTESVVFDPARSVTALLPPHPKNGPTLQEBMKSYKTLITLYLIV 60
QY 61 FVVLVPIIIGIYVAOQLKWKETKCTGVSVNADISPSPEKGNGSEDEMRPREAVMERMSNM 120
DB 61 FVVLVPIIIGIYVAOQLKWKETKCTGVSVNADISPSPEKGNGSEDEMRPREAVMERMSNM 120
QY 121 ESRIOYLSDNENANLDAKNFQNSITTDORFNDVLFQNSLLSSIOEHENIIGDISKSLIV 180
DB 121 ESRIOYLSDNENANLDAKNFQNSITTDORFNDVLFQNSLLSSIOEHENIIGDISKSLIV 180
QY 181 GIANTVLDLQFSIETLNGRVQENAFKQOEEMKLEERIYNASAEIKSLDEKQVLYEOEIK 240
DB 181 GIANTVLDLQFSIETLNGRVQENAFKQOEEMKLEERIYNASAEIKSLDEKQVLYEOEIK 240
QY 241 GEMKLNITNDRLKDMHESQTLKNITLLOG 272
DB 241 GEMKLNITNDRLKDMHESQTLKNITLLOG 272

RESULT 5

ID AAM19708 standard; protein; 451 AA.

XX AAM19708;

XX 19-AUG-1997 (first entry)

DE Macrophage scavenger receptor protein.

KM Macrophage scavenger receptor protein; MSRP; human; lipoteichoic acid;
KW LTA; Gram-positive bacteria; cell wall; atherosclerosis; host defence;

KM septicemia; inhibitor; complement activation; cytokine release; therapy;
XX nitric oxide production; bacterial infection; septic shock.
OS Homo sapiens.
XX US624904-A.
XX 29-APR-1997.
PD 17-NOV-1993; 93US-00154365.
XX 17-NOV-1993; 93US-00154365.
XX 17-NOV-1993; 93US-00154365.
XX 17-NOV-1993; 93US-00154365.
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
PA (UYVA) UNIV YALE.
XX Krieger M, Joiner KA;
XX MPI; 1997-258236/23.
DR N-PSDB; AAT68796.
XX
XX Treatment of septicemia caused by Gram-positive bacteria - by
PT administration of macrophage scavenger receptor protein.
XX
XX Disclosure; Col 23-26; 16pp; English.
XX
XX This sequence represents the human macrophage scavenger receptor protein
CC (MSRP). MSRP binds specifically to the lipoteichoic acid (LTA) residues
CC on the Gram-positive bacterial cell wall. MSRP exhibit unusually broad
CC binding specificity for polyanionic ligands, and have been implicated in
CC atherosclerosis and a variety of host defence functions. This protein is
CC be used in the method of the invention. The method of the invention is
CC for the treatment of septicemia caused by Gram-positive bacteria. The
CC method comprises administration of a MSRP in an amount sufficient to
CC inhibit complement activation, cytokine release or nitric oxide
CC production induced by LTA released by the Gram-positive bacteria. In
CC addition to treating Gram-positive septic shock, the MSRP can be used to
CC screen for other compounds for treating Gram-positive septic shock. MSRP
CC can also be used to purify, label or detect LTA or LTA-containing cells.
CC MSRP, active MSRP fragments, anti-MSRP antibodies or other compounds that
CC inhibit binding of Gram-positive bacteria to MSRP can be used to treat
CC pathologies such as septicemia, Gram-positive bacterial infection, Gram-
CC positive septicemia or Gram-positive or Gram-negative septic shock
XX
XX
SQ Sequence 451 AA;
Query Match 50.9%; Score 1047.5; DB 2; Length 451;
Best Local Similarity 72.5%; Pred. No. 2.7e-75;
Matches 198; Conservative 40; Mismatches 34; Indels 1; Gaps 1;
QY 1 MAQMDPFDQOEDTDSCTESYKFPDARSVTALLPFPKKGPTLOERMKSYKTALITLYIV 60
DB 1 MEQMDHFNQOEDTDSCTESYKFPDARSVTALLPFPKKGPTLOERMKSYKTALITLYIV 60
QY 61 FVVLVPIIGIYAAQLKMETKNCVGSVNA-DISBPBGKNGSEDEMRPREAVMERMSN 119
DB 61 FAVLIPILIGIYAAQLKMETKNCVGSSTNANDITQSLTGKGNDSBEEMRFOEAFMEHMSN 120
QY 120 MESRIQYISDNEAULDAKNFONRISITTDORPNVLPFLNLLSSIOGHENITGDISKL 179
DB 121 MEKRIQHLDMEANLMDTEHFONFSMTTDORFNIDLLQSLTFLSSVOEHENALIDEISKSL 180
QY 180 VGLMTTVYLDLQFSIETTLNGRVOENAFKQOEMRKLEERIYASAEIKSLDKQVYLEQEI 239
DB 181 ISLMTTLLDLOLANTENANGKIQENTFKQOERISKLEERVYVSAEIMAMEGQVHLBEI 240
QY 240 KGEKMLNNTITNDRLKDMESHSQTLKNITLLQG 272
DB 241 KGEVYVLIANNITNDRLKDMESHSQTLKNITLLQG 273
RESULT 6
AD162129

ID AD162129 standard; protein; 451 AA.
XX
XX AD162129;
AC
XX 15-APR-2004 (first entry)
DT
XX Human macrophage scavenger receptor protein 1 mutant V113A.
DE
XX prostatic cancer; asthma; cardiovascular disease;
XX macrophage scavenger receptor protein 1; MSRI; human; receptor; mutant;
KM
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
FH Key location/Qualifiers
FT Misc-difference 113 /note= "Wild type Val substituted by Ala"
FT
XX
XX US2004018521-A1.
XX
XX 29-JAN-2004.
XX
XX 30-APR-2003; 2003US-00426262.
XX
XX 07-MAY-2002; 2002US-0378377P.
XX
XX (XUJ/) XU J.
PA (MEYER/) MEYERS D.
PA (ZHEN/) ZHENG S.
PA (WALS/) WALSH P C.
PA (ISAA/) ISAACS W B.
PA (BLEE/) BLEECKER E.
PA (HERR/) HERRINGTON D.
XX
XX Xu J, Meyer D, Zheng S, Walsh PC, Isaacs WB, Bleecker E;
PI Herrington D;
XX
XX MPI; 2004-122024/12.
XX
XX Screening a subject for increased risk of prostate cancer or asthma, or
PT decreased risk of cardiovascular disease by detecting the presence or
PT absence of an MSRI mutation in the subject.
XX
XX
PS Claim 1; Page; 21pp; English.
XX
XX The invention describes a method of screening a subject for increased
CC risk of prostate cancer or asthma, or decreased risk of cardiovascular
CC disease. The method comprises: detecting the presence or absence of an
CC MSRI mutation in the subject; and determining that the subject is at
CC increased risk of prostate cancer, increased risk of asthma, or decreased
CC risk of cardiovascular disease due to the presence or absence of the MSRI
CC mutation consisting of H441R, G369S, R293X, P275A, D174Y, V113A, S41Y,
CC P36A or 154V. The method is useful for screening a subject for increased
CC risk of prostate cancer or asthma, or decreased risk of cardiovascular
CC disease. This is the amino acid sequence of a human macrophage scavenger
CC protein 1 (MSRI) mutant of the invention. Note: This sequence does not
CC appear in the printed specification but has been created using
CC information given in the specification.
XX
SQ Sequence 451 AA;
Query Match 50.8%; Score 1046.5; DB 8; Length 451;
Best Local Similarity 72.5%; Pred. No. 3.3e-75;
Matches 198; Conservative 41; Mismatches 33; Indels 1; Gaps 1;
QY 1 MAQMDPFDQOEDTDSCTESYKFPDARSVTALLPFPKKGPTLOERMKSYKTALITLYIV 60
DB 1 MEQMDHFNQOEDTDSCTESYKFPDARSVTALLPFPKKGPTLOERMKSYKTALITLYIV 60
QY 61 FVVLVPIIGIYAAQLKMETKNCVGSVNA-DISBPBGKNGSEDEMRPREAVMERMSN 119
DB 61 FAVLIPILIGIYAAQLKMETKNCVGSSTNANDITQSLTGKGNDSBEEMRFOEAFMEHMSN 120

QY 120 MESRIQYLSDEANLIDAKNFQNFSTTDDRFNDVLPQNLSSLOEHENIIGDISKL 179
 DB 121 MEKRIQHLIDMEANLIDTEHFQNFSTTDDRFNDILQSTLPSVQGHGNAIDETSKL 180
 QY 180 VGLNTTVLDLPQSIETLNGRVOENAFKQOEBMKLEERLYNASAEIKSLDEKQVYLEOEI 239
 DB 181 ISLNTTLLDLPQNTENLNGKIQENTPFKQOEBISKLEERYVNASAEIMAKKEQVHLEOEI 240
 QY 240 KGEMLNNITNDLRKQWESHQTLKNITLLQG 272
 DB 241 KGEVAVLNNITNDLRKQWESHQTLKNITLLQG 273

RESULT 7

AAK21513
 ID AAK21513 standard; protein; 358 AA.

XX AAK21513;
 AC AAR21513;
 XX 25-MAR-2003 (revised)
 DT 19-MAY-1992 (first entry)
 XX Human scavenger receptor type II.
 DE Human scavenger receptor type II.
 XX Lipoproteins.
 OS Homo sapiens.
 XX JP03290184-A.
 XX 19-DEC-1991.
 PD 06-APR-1990; 90JP-00090274.
 PF 06-APR-1990; 90JP-00090274.
 PR 06-APR-1990; 90JP-00090274.
 XX (CHUS) CHUGAI PHARM CO LTD.
 PA WPI; 1992-051436/07.
 DR N-PSDB; AAQ21550.
 XX New scavenger receptor-producing animal cells - which have been
 PT transformed with vector contg. gene for coding human scavenger receptor I
 or II type under control of promoter, etc.
 XX Discloure; Fig 2; 9pp; Japanese.
 PS The gene encoding the receptor can be expressed from a cytomogalo- virus
 CC promoter in a host cell e.g. CHO cell. The resulting recombinant
 CC scavenger receptor can be used to detect modified lipo- proteins or
 CC modified substances in the blood. See also AAK21512. (Updated on 25-MAR-
 CC 2003 to correct PA field.)
 XX
 SQ Sequence 358 AA;

Query Match 50.6%; Score 1042.5; DB 2; Length 358;

Best Local Similarity 72.2%; Pred. No. 4.9e-75;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAOWDDPPOQEDTSCSVEKFDARSVTALPPHPKNGPTLOERKSYKATLITLYLV 60
 DB 1 MEQWHFHQQEDTSCSVEKFDARSMTALPPHPKNSPSLOEKLSKAKALLIYLYLV 60
 QY 61 FVVLVPIIGIIVAQAOLKMETKNCVGSVNA-DISPSPEKNGSGSEDEMFRFAVNERMSN 119
 DB 61 FAVLLPLIGIIVAQAOLKMETKNCVGSVNA-DISPSPEKNGSGSEDEMFRFAVNERMSN 120
 QY 120 MESRIQYLSDEANLIDAKNFQNFSTTDDRFNDVLPQNLSSLOEHENIIGDISKL 179
 DB 121 MEKRIQHLIDMEANLIDTEHFQNFSTTDDRFNDILQSTLPSVQGHGNAIDETSKL 180
 QY 180 VGLNTTVLDLPQSIETLNGRVOENAFKQOEBMKLEERLYNASAEIKSLDEKQVYLEOEI 239
 DB 181 ISLNTTLLDLPQNTENLNGKIQENTPFKQOEBISKLEERYVNASAEIMAKKEQVHLEOEI 240

DB 181 ISLNTTLLDLPQNTENLNGKIQENTPFKQOEBISKLEERYVNASAEIMAKKEQVHLEOEI 240
 QY 240 KGEMLNNITNDLRKQWESHQTLKNITLLQG 272
 DB 241 KGEVAVLNNITNDLRKQWESHQTLKNITLLQG 273

RESULT 8

AAK40803
 ID AAK40803 standard; protein; 358 AA.

XX AAK40803;
 AC AAR40803;
 XX 23-FEB-1994 (first entry)
 DT Human scavenger receptor II.
 XX Human; scavenger receptor; antihuman scavenger receptor antibody; AHSRA;
 KW mammal; rabbit; antiserum; monoclonal; HAT-resistant hybridoma;
 XX arteriosclerosis.
 OS Homo sapiens.
 XX JP05192179-A.
 XX 03-AUG-1993.
 PD 16-AUG-1991; 91JP-00229728.
 PF 27-AUG-1990; 90JP-00222398.
 PR (CHUS) CHUGAI PHARM CO LTD.
 PA WPI; 1993-277488/35.
 DR N-PSDB; AAQ47731.
 XX Anti-human scavenger receptor antibody - useful for monitoring progress
 PT of arteriosclerosis.
 PS Claim 2; Page 7-9; 10pp; Japanese.
 CC The sequences given in AAK40802-03 represent the human scavenger
 CC receptors I and II. These proteins may be used in the production of
 CC antihuman scavenger receptor antibodies (AHSRA). These peptides were used
 CC to immunise a mammal, pref. a rabbit, and anti-serum was prepared. A
 CC monoclonal antibody was prepared from HAT-resistant hybridoma. These
 CC antibodies may be used to determine the progress of arteriosclerosis
 XX
 SQ Sequence 358 AA;

Query Match 50.6%; Score 1042.5; DB 2; Length 358;

Best Local Similarity 72.2%; Pred. No. 4.9e-75;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAOWDDPPOQEDTSCSVEKFDARSVTALPPHPKNGPTLOERKSYKATLITLYLV 60
 DB 1 MEQWHFHQQEDTSCSVEKFDARSMTALPPHPKNSPSLOEKLSKAKALLIYLYLV 60
 QY 61 FVVLVPIIGIIVAQAOLKMETKNCVGSVNA-DISPSPEKNGSGSEDEMFRFAVNERMSN 119
 DB 61 FAVLLPLIGIIVAQAOLKMETKNCVGSVNA-DISPSPEKNGSGSEDEMFRFAVNERMSN 120
 QY 120 MESRIQYLSDEANLIDAKNFQNFSTTDDRFNDVLPQNLSSLOEHENIIGDISKL 179
 DB 121 MEKRIQHLIDMEANLIDTEHFQNFSTTDDRFNDILQSTLPSVQGHGNAIDETSKL 180
 QY 180 VGLNTTVLDLPQSIETLNGRVOENAFKQOEBMKLEERLYNASAEIKSLDEKQVYLEOEI 239
 DB 181 ISLNTTLLDLPQNTENLNGKIQENTPFKQOEBISKLEERYVNASAEIMAKKEQVHLEOEI 240
 QY 240 KGEMLNNITNDLRKQWESHQTLKNITLLQG 272

Db 241 KGEVKVLLNNTNDLRLKDMHSQTLRNITLLIOG 273

RESULT 9

AAW08078 ID AAW08078 standard; protein; 358 AA.

XX AC AAW08078;

XX DT 25-FEB-1997 (first entry)

XX DE Type II macrophage scavenger receptor.

XX DE Type II macrophage scavenger receptor; SRG; kidney; 293 cell;

XX KM cell substrate; cell attachment; atherosclerosis.

XX OS Homo sapiens.

XX PN M09638725-A1.

XX PD 05-DEC-1996.

XX PF 30-MAY-1996; 96WO-US008081.

XX PR 30-MAY-1995; 95US-00453117.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX P1 Lyoko PG, Elshourbagy NAE, Brawner ME;

XX DR WPI; 1997-034505/03.

XX DR N-PSDB; AAT43260.

XX PT New modified human embryonic kidney 293 cells - transfected with a

XX PT mammalian scavenger receptor gene to enhance ability to attach to a solid

XX PT support.

XX PS Disclosure; Page 16-18; 32pp; English.

XX CC Human type I (AAW08077) and type II (AAW08078) macrophage scavenger

XX CC receptors can be expressed in human embryonic kidney 293 cells following

XX CC transfection of the cells with vectors carrying the respective scavenger

XX CC receptor genes (AAT43259 and AAT43260). The transfected cells show an

XX CC enhanced ability to attach to a solid support and are useful for

XX CC screening cpds. for biological activity, or for identifying antagonists

XX CC of the scavenger receptor gene, e.g. to develop agents for treatment of

XX CC atherosclerosis

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RESULT 10

ABAB49716 ID ABAB49716 standard; protein; 358 AA.

XX AC ABAB49716;

XX DT 05-APR-2001 (first entry)

XX DE Human type II scavenger receptor amino acid sequence.

XX DE Human; type II scavenger receptor; antibody; macrophage.

XX OS Homo sapiens.

XX PN JP2000312595-A.

XX PD 14-NOV-2000.

XX PF 16-AUG-1991; 2000JP-00114233.

XX PR 27-AUG-1990; 90JP-00222398.

XX PR 16-AUG-1991; 91JP-00229728.

XX PA (CHUS) CHUGAI PHARM CO LTD.

XX DR WPI; 2001-161981/17.

XX DR N-PSDB; AAF29165.

XX PT New anti-human scavenger receptor antibody useful for the identification

XX PT and the determination of macrophages.

XX PS Claim 1; Page 7-9; 13pp; Japanese.

XX CC This invention relates to a polyclonal or monoclonal antibody which targets a

XX CC human type I or type II scavenger receptor epitope. The anti-scavenger

XX CC receptor antibody can be used for the identification and determination of

XX CC macrophages. The present sequence represents the human type II scavenger

XX CC receptor protein, to which the antibody of the invention is directed

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RESULT 11

ADB89003 ID ADB89003 standard; protein; 358 AA.

XX AC ADB89003;

XX DT 05-APR-2001 (first entry)

XX DE Human type II scavenger receptor amino acid sequence.

XX DE Human; type II scavenger receptor; antibody; macrophage.

XX OS Homo sapiens.

XX PN JP2000312595-A.

XX PD 14-NOV-2000.

XX PF 16-AUG-1991; 2000JP-00114233.

XX PR 27-AUG-1990; 90JP-00222398.

XX PR 16-AUG-1991; 91JP-00229728.

XX PA (CHUS) CHUGAI PHARM CO LTD.

XX DR WPI; 2001-161981/17.

XX DR N-PSDB; AAF29165.

XX PT New anti-human scavenger receptor antibody useful for the identification

XX PT and the determination of macrophages.

XX PS Claim 1; Page 7-9; 13pp; Japanese.

XX CC This invention relates to a polyclonal or monoclonal antibody which targets a

XX CC human type I or type II scavenger receptor epitope. The anti-scavenger

XX CC receptor antibody can be used for the identification and determination of

XX CC macrophages. The present sequence represents the human type II scavenger

XX CC receptor protein, to which the antibody of the invention is directed

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DT	18-DEC-2003	(first entry)
XX	Human macrophage scavenging receptor.	
XX	Human macrophage scavenging receptor; heptad repeat;	
XX	reduced immunogenicity; trimerisation; CD40L; immune response;	
XX	T-cell activation; isotype switching.	
XX	Homo sapiens.	
XX	Key	
XX	Location/Qualifiers	
XX	96..244	
XX	/note="This region is specifically claimed in claim 14,	
XX	but since the authors have confused the descriptions of	
XX	the sequences as they appear in the figure, the indexer	
XX	cannot correctly assign a function to this region"	
XX	US2003119149-A1.	
XX	26-JUN-2003.	
XX	20-DEC-2002; 2002US-00326186.	
XX	21-DEC-2001; 2001US-0343315P.	
XX	(REDD/) REDDY P.	
XX	Reddy P;	
XX	WPI, 2003-863437/80.	
XX	N-PsDB; ADB89012.	
XX	New fusion polypeptide that is capable of forming a trimer, useful in	
XX	preparing a composition for treating immune related or inflammatory	
XX	disorders.	
XX	Claim 14; Fig 4; 24pp; English.	
XX	The present invention relates to a polypeptide comprising a fusion	
XX	protein capable of forming a trimer and comprising a heptad repeat	
XX	containing region of the human macrophage scavenging factor protein	
XX	appearing as ADB89007 fused to a second protein (especially a member of	
XX	the tumour necrosis superfamily, TNFSF e.g. CD40L). CD40L is involved in	
XX	isotype switching and is important in T-cell activation in the immune	
XX	response. The fusion protein has reduced immunogenicity due to its	
XX	ability to form trimers. Also included are the nucleic acids encoding the	
XX	fusion proteins, host cells comprising the nucleic acids (used to produce	
XX	the fusion protein) and a recombinant vector comprising the nucleic acid.	
XX	The fusion proteins are used to deliver a therapeutic protein with	
XX	reduced immunogenicity to a patient in need of the protein. The present	
XX	sequence represents the human macrophage scavenging factor protein. Note:	
XX	The authors have mixed up the descriptions of the sequences as they	
XX	appear in the figures, therefore there is a possibility that the	
XX	description assigned by the indexer may be wrong.	
XX	Sequence 358 AA;	
XX	Query Match 50.6%; Score 1042.5; DB 7; Length 358;	
XX	Best local similarity 72.2%; Pred. No. 4,9e-75;	
XX	Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1	
QY	1 MAQWDDPDDQEDTDSCTESVFKFARSVTALLPFPKNGPTLOERMKSXTALITLYLIV 60	
DB	1 MEQWQHFNQGDJDSCTESVFKFARSMVALLPFPKNSPSIQEKTKSRKALLINLYLIV 60	
QY	61 FVLTVPITIGIVAQLIKWETKNCVGSVNA-DISPSPEKNGSGSEDEMFRRAVVERMSN 119	
DB	61 FAVLIPITIGIVAQLIKWETKNCVGSSTVANDITQSLTSGKNDSEEMKRFQEVMEHMSN 120	
QY	120 MESRTQYLSNDNANLLDAKNGPFGSTTDQRNDVLPQLNSLSSIQEHNITIGDISKL 179	
DB	121 MEKRTQHLIDNEANILMDTEHFQNFSTWTDQRENDIILQISTLFSSVQGGNAIDETSKL 180	

[illegible]

CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 358 AA;

Qy Query Match 50.6%; Score 1042.5; DB 8; Length 358;
Best Local Similarity 72.2%; Pred. No. 4.9e-75;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

1 MAQWDDPPDOQEDTSCESYKFPDARSVTALLPPHKNKGPFLQERMSYKTAITLYLIY 60

1 MEQWDHFNHQEDTSCESYKFPDARSMTALLPPHKNKSPSLQKLSFKKALITLYLIY 60

61 FVVLVPIIIGIYAAQLKMETKNCVGSVNA-DISPEPGKNGSEDEMRFEAVMERHNS 119

61 FAVLIPILIGIYAAQLKMETKNCVGSSTNANDITQSLTGKNDSEEMRFQEVMEHNSN 120

120 MESRIQYLSDEANLILDAKNFQNFSTTDOGFNDVLFQNLNLSIOEHENIIGDISKSL 179

121 MEKRIQHLDEANLIMDTHEHFQNFMTTDOGFNDILQSLTFSVQGHGAIDKISKL 180

180 VGLNTTVLDLQFSIETLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVYLEGEI 239

181 ISLNTTLLDQLNTENLNKIQENTFKQOEISKLEERVYVNSAEMAMKEEQVHLEGEI 240

240 KGEVKLNNTITNDLRKDWHSQTLRNITLLOG 272

241 KGEVKLNNTITNDLRKDWHSQTLRNITLLOG 273

ADQ39731 standard; protein; 358 AA.

ADQ39731

ADQ39731; (first entry)

18-NOV-2004

Human myocardial infarction-associated gene derived protein, SEQ ID 1394.

Myocardial infarction; detection; single nucleotide polymorphism; SNP;

cardiant; gene therapy; human.

Homo sapiens.

MO2004058052-A2.

15-JUL-2004.

22-DEC-2003; 2003WO-US040978.

20-DEC-2002; 2002US-0434778P.

10-MAR-2003; 2003US-0451135P.

30-APR-2003; 2003US-0466412P.

23-SEP-2003; 2003US-0504955P.

(APPL-) APPLERA CORP.

Cargill M, Devlin J, Iakubova O;

WPI; 2004-533949/51.

N-PDB; ADQ38903.

Identifying an individual who has an altered risk for developing

myocardial infarction by detecting a single nucleotide polymorphism in

the individual's nucleic acids.

Claim 10; SEQ ID NO 1394; 145pp; English.

The invention relates to a novel method for identifying an individual who

has an altered risk for developing myocardial infarction. The method

comprises detecting a single nucleotide polymorphism (SNP) in any one of

CC the nucleotide sequences given in the specification in the individual's

CC nucleic acids, where the presence of the SNP is correlated with an

CC altered risk for myocardial infarction in the individual. The invention

CC further comprises: an isolated nucleic acid molecule comprising at least

CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in

CC the specification or its complement and encoding any one of the amino

CC acid sequences given in the specification; an isolated polypeptide

CC comprising an amino acid sequence given in the specification; an antibody

CC that specifically binds to the polypeptide or its antigen-binding

CC fragment; an amplified polynucleotide containing an SNP given in the

CC specification and which is between about 15 and 1000 nucleotides in

CC length; a kit for detecting an SNP in a nucleic acid, comprising the

CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a

CC nucleic acid molecule; a method of detecting a variant polypeptide; and a

CC method for identifying an agent useful in treating or preventing

CC myocardial infarction. The novel detection method has cardiant activity.

CC The nucleic acids of the invention may be used in gene therapy. The

CC method is useful in identifying an individual who has an increased or

CC decreased risk for developing myocardial infarction and for preparing a

CC composition for treating or preventing myocardial infarction. This

CC sequence represents the protein of a human myocardial infarction-

CC associated gene containing one or more SNP's of the invention. Note: This

CC sequence was not shown in the specification. The sequence has come from

CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 358 AA;

Qy Query Match 50.6%; Score 1042.5; DB 8; Length 358;

Best Local Similarity 72.2%; Pred. No. 4.9e-75; Indels 1; Gaps 1;

Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

1 MAQWDDPPDOQEDTSCESYKFPDARSVTALLPPHKNKGPFLQERMSYKTAITLYLIY 60

1 MEQWDHFNHQEDTSCESYKFPDARSMTALLPPHKNKSPSLQKLSFKKALITLYLIY 60

61 FVVLVPIIIGIYAAQLKMETKNCVGSVNA-DISPEPGKNGSEDEMRFEAVMERHNS 119

61 FAVLIPILIGIYAAQLKMETKNCVGSSTNANDITQSLTGKNDSEEMRFQEVMEHNSN 120

120 MESRIQYLSDEANLILDAKNFQNFSTTDOGFNDVLFQNLNLSIOEHENIIGDISKSL 179

121 MEKRIQHLDEANLIMDTHEHFQNFMTTDOGFNDILQSLTFSVQGHGAIDKISKL 180

180 VGLNTTVLDLQFSIETLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVYLEGEI 239

181 ISLNTTLLDQLNTENLNKIQENTFKQOEISKLEERVYVNSAEMAMKEEQVHLEGEI 240

240 KGEVKLNNTITNDLRKDWHSQTLRNITLLOG 272

241 KGEVKLNNTITNDLRKDWHSQTLRNITLLOG 273

ADQ39734 standard; protein; 358 AA.

ADQ39734

ADQ39734; (first entry)

18-NOV-2004

Human myocardial infarction-associated gene derived protein, SEQ ID 1397.

Myocardial infarction; detection; single nucleotide polymorphism; SNP;

cardiant; gene therapy; human.

Homo sapiens.

MO2004058052-A2.

15-JUL-2004.

22-DEC-2003; 2003WO-US040978.

20-DEC-2002; 2002US-0434778P.

10-MAR-2003; 2003US-0451135P.

30-APR-2003; 2003US-0466412P.

23-SEP-2003; 2003US-0504955P.

(APPL-) APPLERA CORP.

Cargill M, Devlin J, Iakubova O;

WPI; 2004-533949/51.

N-PDB; ADQ38903.

Identifying an individual who has an altered risk for developing

myocardial infarction by detecting a single nucleotide polymorphism in

the individual's nucleic acids.

Claim 10; SEQ ID NO 1394; 145pp; English.

The invention relates to a novel method for identifying an individual who

has an altered risk for developing myocardial infarction. The method

comprises detecting a single nucleotide polymorphism (SNP) in any one of

20-DEC-2002; 2002US-0434778P.
 10-MAR-2003; 2003US-0453135P.
 30-APR-2003; 2003US-0466412P.
 23-SEP-2003; 2003US-0504955P.

(APPL-) APPLERA CORP.

Cargill M, Devlin J, Iakubova O;

WPI; 2004-533949/51.

N-PSDB; ADQ38906.

Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.

Claim 10; SEQ ID NO 1397; 145pp; English.

The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-associated gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

Sequence 358 AA;

Query Match 50.6%; Score 1042.5; DB 8; Length 358;

Best Local Similarity 72.2%; Pred. No. 4.9e-75; Mismatches 34; Indels 1; Gaps 1;

Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

1 MAOWDPDQOEDTSCTESVFPDARSVALPPEPKNGPTLOBRKSKYKALITLYLV 60
 1 MEQWDFHNOQEDTSCSESVPDARSMTALPPPKNSPSLQEXLKSFKALITLYLV 60
 61 FVVLVPIIGIYVAQAOLKWKETKCTGVSVA-DISSPEKKGSGEDENRFRFAVEMKSN 119
 61 FAVLPLGIYVAQAOLKWKETKCSVSSTVANDITSLTGKNGDSEEMKFOEVEFMEHNS 120
 120 MESRIQVSDNEANLDAKNPNSITTDORFNDVLPOLNSLSIOEHENIGISKSL 179
 121 MEKRIQHLIDMEANLMDTEHFNFSMTDORFNDVLPOLNSLSIOEHENIGISKSL 180
 180 VGLNTVLVDFPSITLNGRVOENAFKQOENRKLBERLYNNAASIKSLDEKQVYLBQEI 239
 181 ISLNTLLDQLQNTINENKIOENTFKQOEBISKLEBRVYVSAIIMAKKEQVHLEQEI 240
 240 KGEMLANNITTDALFKMEHSQTKNTLLQ 272
 241 KGEVAVLNNITTDALFKMEHSQTKNTLLQ 273

RESULT 15

ADQ39733

ID ADQ39733 standard; protein; 388 AA.

ADQ39733;

18-NOV-2004 (first entry)

Human myocardial infarction-associated gene derived protein, SEQ ID 1396.

Myocardial infarction; detection; single nucleotide polymorphism; SNP;

cardiant; gene therapy; human.

Homo sapiens.

WO2004058052-A2.

15-JUL-2004.

22-DEC-2003; 2003WO-US040978.

20-DEC-2002; 2002US-0434778P.

10-MAR-2003; 2003US-0453135P.

30-APR-2003; 2003US-0466412P.

23-SEP-2003; 2003US-0504955P.

(APPL-) APPLERA CORP.

Cargill M, Devlin J, Iakubova O;

WPI; 2004-533949/51.

N-PSDB; ADQ38906.

Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.

Claim 10; SEQ ID NO 1396; 145pp; English.

The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-associated gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

Sequence 388 AA;

Query Match 50.6%; Score 1042.5; DB 8; Length 388;

Best Local Similarity 72.2%; Pred. No. 5.5e-75; Mismatches 34; Indels 1; Gaps 1;

Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy	1	MAQWDDFPDQOEDTDSCTESYKFDARSVTALLPPHKNKGPYLQERMKSYKTALITLYLIV	60
Db	1	MEQMDHFNQOEDTDSCTESYKFDARSVTALLPPHKNKGPYLQERMKSYKTALITLYLIV	60
Qy	61	FVVLVPIIGIIVAQOLKMETKNCCTVGSVNA-DISPSPEKNGSGEDEMRFREAVMERMSN	119
Db	61	FVVLVPIIGIIVAQOLKMETKNCCTVGSVNA-DISPSPEKNGSGEDEMRFREAVMERMSN	120
Qy	120	MESRIQYLSDEANLILDAKNFONFSITTDORFNDVLPOLNSLSSIOEHENIIGDISKSL	179
Db	121	MEKRIQHILDEANLILDAKNFONFSITTDORFNDVLPOLNSLSSIOEHENIIGDISKSL	180
Qy	180	VGLNTTVLDELQSIETTLNGRVOENAFKQOEMRKLEERIVNASAEIKSLDERKOVYLEQEI	239
Db	181	ISLNTTLLDLQENIENANGKIQENTFKQOEISKLEERVYVNSAEIMAKREQVHLEQEI	240
Qy	240	KGEMKLNNITNDLRLKDMESHQTLKNITLLQG	272
Db	241	KGEVYKVLNNITNDLRLKDMESHQTLKNITLLQG	273

Search completed: February 16, 2006, 17:01:04
 Job time : 189 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2006, 17:01:22 ; Search time 40 seconds
(without alignments)
962.168 Million cell updates/sec

Title: US-10-618-570-2
Perfect score: 2059
Sequence: 1 MAQMDPDPQOEDTDSCTES.....DKATRVGINFTRLRTQKE 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 40 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1381	67.1	349	2 S08278	macrophage scaveng
2	1381	67.1	453	2 S08276	macrophage scaveng
3	1042.5	50.6	358	2 B38415	macrophage scaveng
4	1042.5	50.6	451	2 A38415	macrophage scaveng
5	994.5	48.3	454	2 A44407	macrophage scaveng
6	987.5	48.0	354	2 I46862	macrophage scaveng
7	987.5	48.0	454	2 I46862	macrophage scaveng
8	801	38.9	350	2 I73338	macrophage scaveng
9	801	38.9	458	2 B44407	macrophage scaveng
10	678	32.9	152	1 VICH	avidin precursor
11	491	22.8	150	2 S42204	avidin-related pro
12	461	22.4	150	2 S42203	avidin-related pro
13	452	22.0	150	2 S42201	avidin-related pro
14	436	21.2	150	2 S42202	avidin-related pro
15	140	6.8	1064	2 A40136	fibropilin Ia - s
16	139.5	6.8	183	2 S57285	streptavidin v2 pr
17	138.5	6.7	183	2 S57284	streptavidin v1 pr
18	138.5	6.7	183	2 A23513	streptavidin precu
19	133.5	6.5	715	2 C70174	methyl-accepting c
20	132.5	6.4	570	2 H97244	membrane associate
21	132.5	6.4	1163	2 G97236	ATPase involved in
22	129.5	6.3	702	2 P97352	CGI protein - huma
23	129.5	6.3	1300	2 I53799	hypothetical prote
24	128.5	6.2	802	2 E91210	hypothetical prote
25	128.5	6.2	802	2 H86056	hypothetical prote
26	128	6.2	833	2 H72205	ORF MSV156 hypothe
27	127.5	6.1	956	2 S30834	hypothetical prote
28	126.5	6.1	956	2 S30834	hypothetical prote
29	126	6.1	1410	1 A57013	early endosome ant

30	124.5	6.0	572	2 T34273	hypothetical prote
31	124.5	6.0	821	2 S67087	hypothetical prote
32	124	6.0	570	2 A48836	fibropilin C prec
33	123.5	6.0	742	2 UC7595	scavenger receptor
34	123.5	6.0	1156	2 B70356	chromosome assembl
35	123	6.0	1009	2 C89910	hypothetical prote
36	123	6.0	2663	1 S28261	centromere protein
37	122.5	5.9	697	2 D84429	hypothetical prote
38	122	5.9	609	2 S46019	YSM1 protein - yea
39	121.5	5.9	320	2 B97206	methyl-accepting c
40	121	5.9	659	2 G82365	methyl-accepting c
41	121	5.9	667	2 B97012	methyl-accepting c
42	120	5.8	1356	2 S32763	kinectin 1 - human
43	119.5	5.8	570	2 A97238	membrane associate
44	119.5	5.8	908	2 AH0055	probable cation-tr
45	119.5	5.8	1265	2 T47626	structural mainten

ALIGNMENTS

RESULT 1
S08278
macrophage scavenger receptor, splice form II - bovine
N:Alternate names: macrophage scavenger receptor type II
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S08278
R:Roehrer, L.; Freeman, M.; Kodama, T.; Penman, M.; Krieger, M.
Nucleotide 343, 570-572, 1990
A:Title: Coiled-coil fibrous domains mediate ligand binding by macrophage scavenger
A:Reference number: S08278; MUID:90136973; PMID:3300208
A:Accession: S08278
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-349 <ROH>
A:Cross-references: UNIPROT:P21758; UNIPARC:UP1000002A6E2; GB:X54183; NID:9736; PIDN:CA
C:Keywords: alternative splicing; coiled coil; glycoprotein; transmembrane protein
F:51-76/Domain: transmembrane #status predicted <TM>
F:82,101,142,183,220,248,266/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 67.1% Score 1381; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 2.8e-79;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAQMDPDPQOEDTDSCTESVFPDARSTALLPFPKXGPTIQERKSKYKTLITLYLV 60
DB	1	MAQMDPDPQOEDTDSCTESVFPDARSTALLPFPKXGPTIQERKSKYKTLITLYLV 60
QY	61	FVVLVPIIGIYVAOQLLKMKETKCTGVSVNADISPSPEKGNGSEDEMRPREAVMERMSNM 120
DB	61	FVVLVPIIGIYVAOQLLKMKETKCTGVSVNADISPSPEKGNGSEDEMRPREAVMERMSNM 120
QY	121	BSRIQYLSDBNEANLLDANKFONFSITTDQRFNDVLFOPLNSLSSIOEHENITGDISKSLV 180
DB	121	BSRIQYLSDBNEANLLDANKFONFSITTDQRFNDVLFOPLNSLSSIOEHENITGDISKSLV 180
QY	181	GIANTVLDIQSFIEFTLNGRVQENAFKQOEEMKLEERLYNAAETIKSLDEKQVYLEQETK 240
DB	181	GIANTVLDIQSFIEFTLNGRVQENAFKQOEEMKLEERLYNAAETIKSLDEKQVYLEQETK 240
QY	241	GEMKLLNNTINDRLKQWHSQTLLKNITLLQG 272
DB	241	GEMKLLNNTINDRLKQWHSQTLLKNITLLQG 272

RESULT 2
S08276
macrophage scavenger receptor, splice form I - bovine
N:Alternate names: macrophage scavenger receptor type I
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S08276

R:Kodama, T.; Freeman, M.; Rohrer, L.; Zabrecky, J.; Matsudaite, P.; Krieger, M.
 Nature 343, 531-535, 1990
 A:Title: Type I macrophage scavenger receptor contains alpha-helical and collagen-like c
 A:Reference number: S08276; MUID:90136665; PMID:2300204
 A:Accession: S08276
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-453 <KOD>
 A:Cross-references: UNIPROT:P21758; UNIPARC:UPI000012F685; GB:X51689; GB:X54182; NID:G73
 A:Note: part of this sequence was confirmed by protein sequencing
 C:Superfamily: macrophage scavenger receptor; scavenger receptor cysteine-rich domain hc
 C:Keywords: alternative splicing; coiled coil; glycoprotein; transmembrane protein
 F:51-76/Domain: transmembrane #status predicted <TM>
 F:349-452/Domain: scavenger receptor cysteine-rich domain homology <SRC>
 F:82,101,142,183,220,248,266/Binding site: carbohydrate (Aan) (covalent) #status predict

Query Match 67.1%; Score 1381; DB 2; Length 453;
 Best Local Similarity 100.0%; Pred. No. 4e-79;
 Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAOMDDPDDQEDPDSCTESVYKFDARSVTALLPFPKNGPTLOERMSKYKTALITLYIV 60
 Db 1 MAOMDDPDDQEDPDSCTESVYKFDARSVTALLPFPKNGPTLOERMSKYKTALITLYIV 60
 Qy 61 FVLVPIIIGIVAAQLKMETKNCCTVGSVNADISPSPEKNGSEDEMERFREAVERMSNM 120
 Db 61 FVLVPIIIGIVAAQLKMETKNCCTVGSVNADISPSPEKNGSEDEMERFREAVERMSNM 120
 Qy 121 ESRIOYLSDEANLIDAKNFQNSITTDQRFNDVLPOLNSLSSIOEHENITIGDISKSLV 180
 Db 121 ESRIOYLSDEANLIDAKNFQNSITTDQRFNDVLPOLNSLSSIOEHENITIGDISKSLV 180
 Qy 181 GIANTVLDLQFSIETLNGRVOENAFKQOEEMRKLEERYNNAEIKSLDEKQVYLEQEI 240
 Db 181 GIANTVLDLQFSIETLNGRVOENAFKQOEEMRKLEERYNNAEIKSLDEKQVYLEQEI 240
 Qy 241 GEMKLNNTNDLRKDWESQTLKNITLLQG 272
 Db 241 GEMKLNNTNDLRKDWESQTLKNITLLQG 272

RESULT 3
 B38415
 A:Title: macrophage scavenger receptor, splice form II - human
 C:Species: Homo sapiens (man)
 C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 09-Jul-2004
 C:Accession: B38415
 R:Matsumoto, A.; Naito, M.; Itakura, H.; Ikemoto, S.; Asaoka, H.; Hayakawa, I.; Kanamori
 man, D.E.; Kodama, T.
 Proc. Natl. Acad. Sci. U.S.A. 87, 9133-9137, 1990
 A:Title: Human macrophage scavenger receptors: primary structure, expression, and local
 A:Reference number: A38415; MUID:91067661; PMID:2251254
 A:Accession: B38415
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-358 <MAT>
 A:Cross-references: UNIPROT:P21757; UNIPARC:UPI000002A663; GB:D90188; NID:G219991; PIDN:
 C:Comment: For an alternative splice form, see PIR:A38415.
 C:Genetics:
 A:Gene: GDB:MSR1
 A:Cross-references: GDB:128046; OMIM:153622
 A:Map position: 8p22-8p22
 C:Superfamily: macrophage scavenger receptor; scavenger receptor cysteine-rich domain hc
 C:Keywords: alternative splicing; coiled coil; transmembrane protein

Query Match 50.6%; Score 1042.5; DB 2; Length 358;
 Best Local Similarity 72.2%; Pred. No. 4.5e-58;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MAOMDDPDDQEDPDSCTESVYKFDARSVTALLPFPKNGPTLOERMSKYKTALITLYIV 60
 Db 1 MAOMDDPDDQEDPDSCTESVYKFDARSVTALLPFPKNGPTLOERMSKYKTALITLYIV 60

Qy 61 FVLVPIIIGIVAAQLKMETKNCCTVGSVNA-DISPSPEKNGSEDEMERFREAVERMSNM 119
 Db 61 FVLVPIIIGIVAAQLKMETKNCCTVGSVNA-DISPSPEKNGSEDEMERFREAVERMSNM 120
 Qy 120 MESRIOYLSDEANLIDAKNFQNSITTDQRFNDVLPOLNSLSSIOEHENITIGDISKSL 179
 Db 120 MESRIOYLSDEANLIDAKNFQNSITTDQRFNDVLPOLNSLSSIOEHENITIGDISKSL 180
 Qy 180 VGLNTVLDLQFSIETLNGRVOENAFKQOEEMRKLEERYNNAEIKSLDEKQVYLEQEI 239
 Db 180 VGLNTVLDLQFSIETLNGRVOENAFKQOEEMRKLEERYNNAEIKSLDEKQVYLEQEI 240
 Qy 240 KGEKLNNTNDLRKDWESQTLKNITLLQG 272
 Db 240 KGEKLNNTNDLRKDWESQTLKNITLLQG 273

RESULT 4
 A38415
 A:Title: macrophage scavenger receptor, splice form I - human
 C:Species: Homo sapiens (man)
 C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 09-Jul-2004
 C:Accession: A38415; A4408
 R:Matsumoto, A.; Naito, M.; Itakura, H.; Ikemoto, S.; Asaoka, H.; Hayakawa, I.; Kanamori
 man, D.E.; Kodama, T.
 Proc. Natl. Acad. Sci. U.S.A. 87, 9133-9137, 1990
 A:Title: Human macrophage scavenger receptors: primary structure, expression, and local
 A:Reference number: A38415; MUID:91067661; PMID:2251254
 A:Accession: A38415
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-451 <MAT>
 A:Cross-references: UNIPROT:P21757; UNIPARC:UPI000012F686; GB:D90187; NID:G219989; PIDN:
 R:Emi, M.; Asaoka, H.; Matsumoto, A.; Itakura, H.; Kurihara, Y.; Wada, Y.; Kanamori, H.;
 J. Biol. Chem. 268, 2120-2125, 1993
 A:Title: Structure, organization, and chromosomal mapping of the human macrophage scav
 A:Reference number: A4408; MUID:93131971; PMID:8093617
 A:Accession: A4408
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 155-272 <EMI>
 A:Cross-references: UNIPARC:UPI0000176ED4
 A:Note: sequence extracted from NCBI backbone (NCBI:P123189)
 C:Comment: For an alternative splice form, see PIR:B38415.
 C:Genetics:
 A:Gene: GDB:MSR1
 A:Cross-references: GDB:128046; OMIM:153622
 A:Map position: 8p22-8p22
 C:Superfamily: macrophage scavenger receptor; scavenger receptor cysteine-rich domain ho
 C:Keywords: alternative splicing; coiled coil; transmembrane protein
 F:347-450/Domain: scavenger receptor cysteine-rich domain homology <SRC>

Query Match 50.6%; Score 1042.5; DB 2; Length 451;
 Best Local Similarity 72.2%; Pred. No. 6.1e-58;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MAOMDDPDDQEDPDSCTESVYKFDARSVTALLPFPKNGPTLOERMSKYKTALITLYIV 60
 Db 1 MAOMDDPDDQEDPDSCTESVYKFDARSVTALLPFPKNGPTLOERMSKYKTALITLYIV 60
 Qy 61 FVLVPIIIGIVAAQLKMETKNCCTVGSVNA-DISPSPEKNGSEDEMERFREAVERMSNM 119
 Db 61 FVLVPIIIGIVAAQLKMETKNCCTVGSVNA-DISPSPEKNGSEDEMERFREAVERMSNM 120
 Qy 120 MESRIOYLSDEANLIDAKNFQNSITTDQRFNDVLPOLNSLSSIOEHENITIGDISKSL 179
 Db 120 MESRIOYLSDEANLIDAKNFQNSITTDQRFNDVLPOLNSLSSIOEHENITIGDISKSL 180
 Qy 180 VGLNTVLDLQFSIETLNGRVOENAFKQOEEMRKLEERYNNAEIKSLDEKQVYLEQEI 239
 Db 180 VGLNTVLDLQFSIETLNGRVOENAFKQOEEMRKLEERYNNAEIKSLDEKQVYLEQEI 240
 Qy 240 KGEKLNNTNDLRKDWESQTLKNITLLQG 272
 Db 240 KGEKLNNTNDLRKDWESQTLKNITLLQG 272

Db 241 KGEVAVLNITNDLRLKQWESQTLRNITLLIOG 273

RESULT 5

A44407

macrophage scavenger receptor, splice form II - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999

C:Accession: A44407

R:Doi, T.; Higashino, K.; Kurihara, Y.; Wada, Y.; Miyazaki, T.; Nakamura, H.; Uesugi, S.

J. Biol. Chem. 268, 2126-2133, 1993

A:Title: Charged collagen structure mediates the recognition of negatively charged macro

A:Reference number: A44407; PMID:93131972; PMID:9380589

A:Accession: A44407

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-454 <DOI>

A:Cross-references: UNIPARC:UPI0000176BD3

A:Experimental source: lung

A:Note: Sequence extracted from NCBI backbone (NCBI:123206)

C:Superfamily: macrophage scavenger receptor; scavenger receptor cysteine-rich domain ho

C:Keywords: alternative splicing

F:350-453/Domain: scavenger receptor cysteine-rich domain homology <SRC>

Query Match 48.3%; Score 994.5; DB 2; Length 454;

Best Local Similarity 69.2%; Pred. No. 6.2e-55; Indels 1; Gaps 1;

Matches 189; Conservative 44; Mismatches 39;

1 MAQMDPFDQEDTSCSSEVFKFARASVTALLPPHPKNGPTLOERKSKYKALITLYLV 60

1 MAQMSFTDQEDTSCSSEVFKFARASVTALLPPHPKNGPTLOERKSKYKALITLYLV 60

61 FVVLPIITIGIAAOLIKMETKCTVGSVNAD-ISPSPGKNGSGEDENRFRFAVMERN 119

61 FAVLPITIAIMAAOLIKMETKCTVGSVNAD-ISPSPGKNGSGEDENRFRFAVMERN 119

61 FAVLPITIAIMAAOLIKMETKCTVGSVNAD-ISPSPGKNGSGEDENRFRFAVMERN 119

120 MESRIQYISDNENANLLDAKFNPSITTDQRENDVLPOLNLSLSIOEHENIIGISKL 179

121 MEKRIQYISDNENANLLDAKFNPSITTDQRENDVLPOLNLSLSIOEHENIIGISKL 180

121 MEKRIQYISDNENANLLDAKFNPSITTDQRENDVLPOLNLSLSIOEHENIIGISKL 180

180 VGLNTTVLDLPISITLNGRVOENAFKQOEEMRKLEERLYNNAASAIKSIDERQVYLEOEI 239

181 ISLNTTLLDLHLVETLVNFKFQENTLKQOEISKLKERVHNASAIMSKEQVHLEOEI 240

240 KGEMLNNITNDLRLKQWESQTLRNITLLIOG 272

241 KREAVLVNITNDLRLKQWESQTLRNITLLIOG 273

Db

RESULT 6

146863

macrophage scavenger receptor, splice form II - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004

C:Accession: I46863

R:Rickel, P.E.; Freeman, M.W.

J. Clin. Invest. 90, 1450-1457, 1992

A:Title: Rabbit aortic smooth muscle cells express inducible macrophage scavenger recept

A:Reference number: I46863; PMID:93016877; PMID:1401078

A:Accession: I46863

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-354 <BIC>

A:Cross-references: UNIPROT:Q05585; UNIPARC:UPI000002AB64; GB:L11692; NID:G165510; PIN:

C:Superfamily: macrophage scavenger receptor; scavenger receptor cysteine-rich domain ho

C:Keywords: alternative splicing

Query Match 48.0%; Score 987.5; DB 2; Length 354;

Best Local Similarity 68.9%; Pred. No. 1.2e-54; Indels 1; Gaps 1;

Matches 188; Conservative 44; Mismatches 40;

1 MAQMDPFDQEDTSCSSEVFKFARASVTALLPPHPKNGPTLOERKSKYKALITLYLV 60

Db 1 MAQMSFTDQEDTSCSSEVFKFARASVTALLPPHPKNGPTLOERKSKYKALITLYLV 60

61 FVVLPIITIGIAAOLIKMETKCTVGSVNAD-ISPSPGKNGSGEDENRFRFAVMERN 119

61 FAVLPITIAIMAAOLIKMETKCTVGSVNAD-ISPSPGKNGSGEDENRFRFAVMERN 120

120 MESRIQYISDNENANLLDAKFNPSITTDQRENDVLPOLNLSLSIOEHENIIGISKL 179

121 MEKRIQYISDNENANLLDAKFNPSITTDQRENDVLPOLNLSLSIOEHENIIGISKL 180

180 VGLNTTVLDLPISITLNGRVOENAFKQOEEMRKLEERLYNNAASAIKSIDERQVYLEOEI 239

181 ISLNTTLLDLHLVETLVNFKFQENTLKQOEISKLKERVHNASAIMSKEQVHLEOEI 240

240 KGEMLNNITNDLRLKQWESQTLRNITLLIOG 272

241 KREAVLVNITNDLRLKQWESQTLRNITLLIOG 273

Db

RESULT 7

146862

macrophage scavenger receptor, splice form I - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004

C:Accession: I46862

R:Rickel, P.E.; Freeman, M.W.

J. Clin. Invest. 90, 1450-1457, 1992

A:Title: Rabbit aortic smooth muscle cells express inducible macrophage scavenger recept

A:Reference number: I46862; PMID:93016877; PMID:1401078

A:Accession: I46862

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-454 <BIC>

A:Cross-references: UNIPROT:Q05585; UNIPARC:UPI000012F667; GB:L11693; NID:G165508; PIN:

C:Superfamily: macrophage scavenger receptor; scavenger receptor cysteine-rich domain ho

C:Keywords: alternative splicing

F:350-453/Domain: scavenger receptor cysteine-rich domain homology <SRC>

Query Match 48.0%; Score 987.5; DB 2; Length 454;

Best Local Similarity 68.9%; Pred. No. 1.7e-54; Indels 1; Gaps 1;

Matches 188; Conservative 44; Mismatches 40;

1 MAQMDPFDQEDTSCSSEVFKFARASVTALLPPHPKNGPTLOERKSKYKALITLYLV 60

1 MAQMSFTDQEDTSCSSEVFKFARASVTALLPPHPKNGPTLOERKSKYKALITLYLV 60

61 FVVLPIITIGIAAOLIKMETKCTVGSVNAD-ISPSPGKNGSGEDENRFRFAVMERN 119

61 FAVLPITIAIMAAOLIKMETKCTVGSVNAD-ISPSPGKNGSGEDENRFRFAVMERN 120

120 MESRIQYISDNENANLLDAKFNPSITTDQRENDVLPOLNLSLSIOEHENIIGISKL 179

121 MEKRIQYISDNENANLLDAKFNPSITTDQRENDVLPOLNLSLSIOEHENIIGISKL 180

180 VGLNTTVLDLPISITLNGRVOENAFKQOEEMRKLEERLYNNAASAIKSIDERQVYLEOEI 239

181 ISLNTTLLDLHLVETLVNFKFQENTLKQOEISKLKERVHNASAIMSKEQVHLEOEI 240

240 KGEMLNNITNDLRLKQWESQTLRNITLLIOG 272

241 KREAVLVNITNDLRLKQWESQTLRNITLLIOG 273

Db

RESULT 8

173338

macrophage scavenger receptor, splice form II - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Oct-1999

C:Accession: I73338; B38260

R:Ashkenas, J.; Penman, M.; Vassile, E.; Acton, S.; Freeman, M.W.; Krieger, M.

J. Lipid Res. 34, 983-1000, 1993

A:Title: Structures and high and low affinity ligand binding properties of murine type I

Query Match 48.0%; Score 987.5; DB 2; Length 454;

Best Local Similarity 68.9%; Pred. No. 1.2e-54; Indels 1; Gaps 1;

Matches 188; Conservative 44; Mismatches 40;

1 MAQMDPFDQEDTSCSSEVFKFARASVTALLPPHPKNGPTLOERKSKYKALITLYLV 60

1 MAQMSFTDQEDTSCSSEVFKFARASVTALLPPHPKNGPTLOERKSKYKALITLYLV 60

61 FVVLPIITIGIAAOLIKMETKCTVGSVNAD-ISPSPGKNGSGEDENRFRFAVMERN 119

A:Reference number: I56334; MUID:93359822; PMID:8394868
A:Accession: I7338
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-350 <RES>
A:Cross-references: UNIPARC:UPI000016385; GB:I04275; NID:9233747; PIDN:AAA39748.1; PID:
R:Freeman, M.; Ashkenas, J.; Rees, D.J.G.; Kingsley, D.M.; Copeland, N.G.; Jenkins, N.A.
Proc. Natl. Acad. Sci. U.S.A. 87, 8810-8814, 1990
A>Title: An ancient, highly conserved family of cysteine-rich protein domains revealed b
A:Reference number: A58260; MUID:91062370; PMID:1978939
A:Accession: B38260
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 345-350 <RES>
A:Cross-references: UNIPARC:UPI0000160CCB; GB:M59446; GB:M36818; NID:g192739; PIDN:AAA37
C:Superfamily: macrophage scavenger receptor; scavenger receptor cysteine-rich domain h
C:Keywords: alternative splicing

Query Match	38.9%	Score 801	DB 2	Length 350
Best Local Similarity	59.4%	Pred. NO. 5.7e-43		
Matches 158	Conservative 4e	Mismatches 60	Indels 2	Gaps 2

[illegible]

RESULT 9
B44407

macrophage scavenger receptor, splice form I - mouse
N/Alternate names: macrophage scavenger receptor type I
C/Species: Mus musculus (house mouse)

C:\Date: 30-Apr-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C:\Accession: B44407; A38260; I56334

R;Doi, T.; Higashino, K.; Kurihara, Y.; Wada, Y.; Miyazaki, T.; Nakamura, H.; Uesugi, S. *J. Biol. Chem.* 268, 2126-2133, 1993

A1>Title: Charged collagen structure mediates the recognition of negatively charged matrix
A1Reference number: A44407; MID:93131972; PMID:8360589

A/Accession: B44407
A/Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid
A;Residues: 1-458 <DOI>

A/Cross-references: UNIPROT:P30204; UNIPARC:UPI00000293B4
A/Experimental source: macrophage-like cell line P388D

A₁Note: sequence extracted from NCBI backbone (NCBI:P:123207)
R.Freeman, M.; Ashkenas, J.; Rees, D.J.G.; Kingsley, D.M.; Copeland, N.G.; Jenkins, N.A.

Proc. Natl. Acad. Sci. U.S.A. 87, 8810-8814, 1990

A/Reference number: A38260; MUID:91062370; PMID:1978933
A/Accession: A38260

A;Status: preliminary
A;Molecule type: mRNA

A;Residues: 349-458 <FRE>
A;Cross-references: UNIPROT

Rishkenas, J.; Penman, M.; Vassile, E.; Acton, S.; Freeman, M.W.; Krieger, M. *J. Lipid Res.* 34, 983-1000, 1993

A, Title: Structures and high and low affinity ligand binding properties of murine type I

A:Reference number: 156334; MWID:93359822; PMID:8394668
A:Accession: 156334
A:Status: preliminary; translated from GB/EMBL/DDDD
A:Molecule type:mRNA
A:Residues: 5-458 <RES>
A:Cross-references: UNIPARC:UPI000016CF2B; GB:104274; NID:g233745; PIDN:AAA39747.1; PID:
C:Superfamily: macrophage scavenger receptor; scavenger receptor cysteine-rich domain ho
C:Keywords: alternative splicing
F:354-457/Domain: scavenger receptor cysteine-rich domain homology <SRC>

Query Match	38.9%	Score 801	DB 2	length 458
Best Local Similarity	59.4%	Pred. No. 8e-43		
Matches 158; Conservative	46	Mismatches	2	Gaps 2

[illegible]

RESULT 10
VICH

avidin precursor [validated] - chicken

C:Species: Gallus gallus (chicken)
C:Date: 24-Apr-1984 #sequence
#revision 04-Nov-1994 #text_change 09-Jul-2004

C;Accession: A54975; A27518; A92093; A92092; A03160
R;Wallen, M.J.; Laukkanen, M.O.; Kulomaa, M.S.

submitted to GenBank, January 1994
A:Description: Sequence of the chicken egg-white avidin gene.

A;Reference number: A54975
A;Accession: A54975

A:Molecule type: DNA
A:Residues: 1-21, 'S'

A/Cross-references: UNIPROT:P02701; UNIPARC:UPI00000170CF8; GB:L27818; NID:g450225; PID:g

A;Note: difference at position 22 may be due to PCR error in gene sequence
R/Cope, M.L.; Keinonen, R.A.; Kristo, P.A.; Connely, O.M.; Beattie, W.G.; Zarucki-Schulz, M.

Nucleic Acids Res. 15, 3595-3606, 1987

A;Reference number: A27518; M01D:87203384; PMID:3575102
A;Accession: A27518

A;Molecule type: mRNA
A;Residues: 1-152 <GDP>

A/Cross-references: UNIPARC:UP100000030A9C; GB:X05343; MID:g630/1; PIDN:CAA28954.1; PID:g
R/Delange, R.J.; Huang, T.S.

J. Biol. Chem. 246, 698-709, 1971

A;Reference number: A920
A;Accession: A92093

A:Molecule type: protein
A:Residues: 25-57, 'T', 59-76, 'E', 78-152

A; Cross-references: UNIPARC:UP100000373A3
A; Experimental source: egg white

A/Note: approximately 50% of the
R/Huang, T.S.; Delange, R.J.

J. Biol. Chem. 246, 6886-6897, 1971

A/Contents: sequences of tryptic peptides
A/Accession: A92092
A/Molecule type: protein
A/Residues: 25-57, T, 59-76, E, 78-152 <DEU2>
A/Cross-references: UNIPARC:UPI00000373A3
R.Livnah, O.; Sussman, J.
A/Reference number: A51448; PDB:2AVI
A/Contents: annotation; X-ray crystallography, 3.0 angstroms, with biotin, residues 27-5
R.Livnah, O.; Beyer, E.A.; Wilchek, M.; Sussman, J.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 5076-5080, 1993
A/Title: Three-dimensional structures of avidin and the avidin-biotin complex.
A/Reference number: A47554; PMID:93281699; PMID:8506353
A/Contents: annotation; X-ray crystallography, 3.0 angstroms
R.Pugliese, L.; Coda, A.; Malcovati, M.; Bolognesi, M.
Submitted to the Brookhaven Protein Data Bank, March 1993
A/Reference number: A51623; PDB:1AVR
A/Contents: annotation; X-ray crystallography, 2.7 angstroms, with biotin, residues 27-5
R.Pugliese, L.; Coda, A.; Malcovati, M.; Bolognesi, M.
Submitted to the Brookhaven Protein Data Bank, March 1993
A/Reference number: A51623; PDB:1AVR
A/Contents: annotation; X-ray crystallography, 2.8 angstroms, without biotin, residues 2
R.Pugliese, L.; Coda, A.; Malcovati, M.; Bolognesi, M.
J. Mol. Biol. 231, 698-710, 1993
A/Title: Three-dimensional structure of the tetragonal crystal form of egg-white avidin
A/Reference number: A54974; PMID:93294833; PMID:8515446
A/Contents: annotation; X-ray crystallography, 2.7 angstroms
C/Genetics:
A/Introns: 27/3; 98/1; 138/2
C/Superfamily: avidin
C/Keywords: glycoprotein
F.1-24/Domain: signal sequence #status predicted <Sig>
F.25-150/Product: signal sequence #status experimental <Mat>
F.28-105/Diulfide bonds: #status experimental
F.41/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 32.9%; Score 678; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 9.6e-36;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 ARKCSLTGKMTNDLSNMITGAVNSRGFTGYITAVTATSNIEKESPLHGQNTINKRT 332
DB 25 ARKCSLTGKMTNDLSNMITGAVNSRGFTGYITAVTATSNIEKESPLHGQNTINKRT 84

QY 333 OPTFGFTVWVKSESTVFTGQCFIDRNGKEVLTMTMLRSSVNDIGDWMKATRVGINF 392
DB 85 OPTFGFTVWVKSESTVFTGQCFIDRNGKEVLTMTMLRSSVNDIGDWMKATRVGINF 144

QY 393 TRLRTQKE 400
DB 145 TRLRTQKE 152

RESULT 11
S42204
Avidin-related protein 4/5 precursor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S42204; S42205
R.Keinaenen, R.A.; Wallen, M.J.; Kristo, P.A.; Laukkanen, M.O.; Toimela, T.A.; Helenius, B.
Eur. J. Biochem. 220, 615-621, 1994
A/Title: Molecular cloning and nucleotide sequence of chicken avidin-related genes 1-5.
A/Reference number: S42201; PMID:94170814; PMID:8125122
A/Accession: S42204
A/Molecule type: DNA
A/Residues: 1-150 <KE1>
A/Cross-references: UNIPROT:P56734; UNIPARC:UPI0000126678; EMBL:Z22883; NID:G311811
A/Experimental source: strain white leghorn; tissue oviduct
A/Genetics: CH1
A/Accession: S42205
A/Molecule type: DNA
A/Residues: 1-150 <KEW>
A/Cross-references: UNIPARC:UPI0000126678; EMBL:Z22882; NID:G311812

A/Experimental source: strain white leghorn; tissue oviduct
A/Genetics: CH2
C/Genetics: <CH1>
A/Gene: avr4
A/Introns: 27/3; 96/1; 136/2
C/Genetics: <CH2>
A/Gene: avr5
A/Introns: 27/3; 96/1; 136/2
C/Superfamily: avidin
F.1-24/Domain: signal sequence #status predicted <Sig>
F.25-150/Product: signal sequence #status predicted <Mat>
F.28-105/Diulfide bonds: #status predicted

Query Match 23.8%; Score 491; DB 2; Length 150;
Best Local Similarity 76.6%; Pred. No. 4.7e-24;
Matches 98; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

QY 273 ARKCSLTGKMTNDLSNMITGAVNSRGFTGYITAVTATSNIEKESPLHGQNTINKRT 332
DB 25 ARKCSLTGKMTNDLSNMITGAVNSRGFTGYITAVADNPNTILSPILGIQH--KRAS 82

QY 333 OPTFGFTVWVKSESTVFTGQCFIDRNGKEVLTMTMLRSSVNDIGDWMKATRVGINF 392
DB 83 OPTFGFTVWVKSESTVFTGQCFIDRNGKEVLTMTMLRSSVNDISYDWMKATRVGINF 142

QY 393 TRLRTQKE 400
DB 143 TRLRTQKE 150

RESULT 12
S42203
Avidin-related protein 3 precursor - chicken
A/Alternate names: avr3 protein
C/Species: Gallus gallus (chicken)
C/Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S42203; S39800
R.Keinaenen, R.A.; Wallen, M.J.; Kristo, P.A.; Laukkanen, M.O.; Toimela, T.A.; Helenius, B.
Eur. J. Biochem. 220, 615-621, 1994
A/Title: Molecular cloning and nucleotide sequence of chicken avidin-related genes 1-5.
A/Reference number: S42201; PMID:94170814; PMID:8125122
A/Accession: S42203
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-150 <KE1>
A/Cross-references: UNIPROT:P56733; UNIPARC:UPI0000126677; EMBL:Z21612; NID:G65432
R.Kunna, T.A.; Wallen, M.J.; Kulomaa, M.S.
Biochem. Biophys. Acta 1216, 441-445, 1993
F.25-150/Product: induction of chicken avidin and related mRNAs after bacterial infection.
A/Reference number: S39799; PMID:94092737; PMID:8268225
A/Accession: S39800
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 71-150 <KUN>
A/Cross-references: UNIPARC:UPI0000178FD; EMBL:Z21536; NID:G65429
C/Genetics:
A/Gene: avr3
A/Introns: 27/3; 96/1; 136/2
C/Superfamily: avidin
F.1-24/Domain: signal sequence #status predicted <Sig>
F.25-150/Product: signal sequence #status predicted <Mat>
F.28-105/Diulfide bonds: #status predicted

Query Match 22.4%; Score 461; DB 2; Length 150;
Best Local Similarity 71.1%; Pred. No. 3.6e-22;
Matches 91; Conservative 10; Mismatches 25; Indels 2; Gaps 1;

QY 273 ARKCSLTGKMTNDLSNMITGAVNSRGFTGYITAVTATSNIEKESPLHGQNTINKRT 332
DB 25 ARKCSLTGKMTNDLSNMITGAVNSRGFTGYITAVADNPNTILSPILGIQH--KRAC 82

QY 333 OPTFGFTVWVKSESTVFTGQCFIDRNGKEVLTMTMLRSSVNDIGDWMKATRVGINF 392
DB 143 TRLRTQKE 150

Db 83 QPTGFTVHWNFSESTSVFVGQCFIDRSKGVLTQRLAVDDISDDWKATRVGVNMF 142
QY 393 TRLRTOKE 400
143 TRQRTVEE 150

RESULT 13
S42201
avidin-related protein 1 precursor - chicken
NAlternate names: avr1
CSpecies: Gallus gallus (chicken)
CDate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
CAccession: S42201
R:Keinanen, R.A.; Wallen, M.J.; Kristo, P.A.; Laukkanen, M.O.; Toimela, T.A.; Helenius, E. J. Biochem. 220, 615-621, 1994
A>Title: Molecular cloning and nucleotide sequence of chicken avidin-related genes 1-5.
A:Reference number: S42201; MUID:94170814; PMID:8125122
A:Accession: S42201
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-150 <KE1>
A:Cross-references: UNIPROT:O13153; UNIPARC:UPI0000126670; EMBL:Z21611
C:Genetics:
A:Introns: 27/3; 96/1; 136/2
C:Superfamily: avidin
C:Keywords: glycoprotein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-150/Product: avidin-related protein 1 #status predicted <MAT>
F:28-105/Disulfide bonds: #status predicted
F:54,67,93/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.0%; Score 452; DB 2; Length 150;
Best Local Similarity 68.8%; Pred. No. 1.3e-21;
Matches 88; Conservative 10; Mismatches 28; Indels 2; Gaps 1;

QY 273 ARKSLTGKMTNDGSMNTIGAVNSRGEFTGYITAVATSNIEKESPLHGTONITNKRT 332
DB 25 ARKSLTGKMTNDGSMNTIGAVNSRGEFTGYITAVADNPQITRSPDLGIQH--KRAS 82

QY 333 OPTGFTVHWNFSESTSVFVGQCFIDRSKGVLTQRLAVDDISDDWKATRVGVNMF 392
DB 83 QPTGFTVHWNFSESTSVFVGQCFIDRSKGVLTQRLAVDDISDDWKATRVGVNMF 142

QY 393 TRLRTOKE 400
143 TRQRTVEE 150

Db 143 TRQRTVEE 150

RESULT 14
S42202
avidin-related protein 2 precursor - chicken
NAlternate names: avr2 protein
CSpecies: Gallus gallus (chicken)
CDate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
CAccession: S42202; S39799
R:Keinanen, R.A.; Wallen, M.J.; Kristo, P.A.; Laukkanen, M.O.; Toimela, T.A.; Helenius, E. J. Biochem. 220, 615-621, 1994
A>Title: Molecular cloning and nucleotide sequence of chicken avidin-related genes 1-5.
A:Reference number: S42202; MUID:94170814; PMID:8125122
A:Accession: S42202
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-150 <KE1>
A:Cross-references: UNIPROT:P56732; UNIPARC:UPI0000000AEB; EMBL:Z21554; NID:g65430
R:Kunam, I.A.; Wallen, M.J.; Kulomaa, M.S.
Biochim. Biophys. Acta 1216, 441-445, 1993
A>Title: Induction of chicken avidin and related mRNAs after bacterial infection.
A:Reference number: S39799; MUID:94092737; PMID:8268225
A:Accession: S39799
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 71-150 <KUN>

A:Cross-references: UNIPARC:UPI00001778FE; EMBL:Z21535; NID:g65428
C:Genetics:
A:Gene: avr2
A:Introns: 27/3; 96/1; 136/2
C:Superfamily: avidin
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-150/Product: avidin-related protein 2 #status predicted <MAT>
F:28-105/Disulfide bonds: #status predicted

Query Match 21.2%; Score 436; DB 2; Length 150;
Best Local Similarity 67.2%; Pred. No. 1.3e-20;
Matches 86; Conservative 11; Mismatches 23; Indels 2; Gaps 1;

QY 273 ARKSLTGKMTNDGSMNTIGAVNSRGEFTGYITAVATSNIEKESPLHGTONITNKRT 332
DB 25 ARKSLTGKMTNDGSMNTIGAVNSRGEFTGYITAVADNPQITRSPDLGIQH--KRAS 82

QY 333 OPTGFTVHWNFSESTSVFVGQCFIDRSKGVLTQRLAVDDISDDWKATRVGVNMF 392
DB 83 QPTGFTVHWNFSESTSVFVGQCFIDRSKGVLTQRLAVDDISDDWKATRVGVNMF 142

QY 393 TRLRTOKE 400
143 TRQRTVEE 150

Db 143 TRQRTVEE 150

RESULT 15
A40136
fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)
NAlternate names: epidermal growth factor homolog precursor
N:Contents: alternatively spliced fibropellin Ib (EGF1)
CSpecies: Strongylocentrotus purpuratus (purple urchin)
CDate: 13-May-1992 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
CAccession: A40136; A40136; A29316; A43131
R:Deigadillo-Reynoso, M.G.; Rollo, D.R.; Hurth, D.A.; Raff, R.A.
J. Mol. Evol. 29, 314-327, 1989
A>Title: Structural analysis of the uEGF gene in the sea urchin Strongylocentrotus purpuratus.
A:Reference number: A40136; MUID:90112459; PMID:2514273
A:Accession: A40136
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-114
A:Cross-references: UNIPROT:P10079; UNIPARC:UPI000016C068; GB:X17530; NID:g10225; PID:g6
A:Accession: A40136
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 181-251, 329-370, 'R', 372-408, 'RA', 411-441 <DE2>
A:Cross-references: UNIPARC:UPI000017BF23
A:Accession: C40136
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 'K', 747-821, 898-978 <DE3>
A:Cross-references: UNIPARC:UPI000017BP23
R:Hurth, D.A.; Andrews, M.E.; Raff, R.A.
Science 237, 1487-1490, 1987
A>Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.
A:Reference number: A29316; MUID:87319677; PMID:3498216
A:Accession: A29316
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 'S', 280-481, 786-1064 <HUR>
A:Cross-references: UNIPARC:UPI000016C06A; GB:M17421; NID:g161474; PID:AAA30050.1; PID:
R:Hunt, L.T.; Barker, W.C.
PSEB J. 3, 1760-1764, 1989
A>Title: Avidin-like domain in an epidermal growth factor homolog from a sea urchin.
A:Reference number: A43131; MUID:85196806; PMID:2784773
A:Contents: annotation
A:Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib)
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1064/Product: fibropellin I #status predicted <FIB>
F:23-54/Domain: EGF homology <EG01>
F:57-175/Domain: C1r/C1s repeat homology <CLR>
F:180-211/Domain: EGF homology <EG02>

F/218-249/Domain: EGF homology <EG03>
 F/256-287/Domain: EGF homology <EG04>
 F/294-325/Domain: EGF homology <EG05>
 F/332-363/Domain: EGF homology <EG06>
 F/370-401/Domain: EGF homology <EG07>
 F/408-439/Domain: EGF homology <EG08>
 F/446-477/Domain: EGF homology <EG09>
 F/484-515/Domain: EGF homology <EG10>
 F/522-553/Domain: EGF homology <EG11>
 F/560-591/Domain: EGF homology <EG12>
 F/598-629/Domain: EGF homology <EG13>
 F/636-667/Domain: EGF homology <EG14>
 F/674-705/Domain: EGF homology <EG15>
 F/712-743/Domain: EGF homology <EG16>
 F/750-781/Domain: EGF homology <EG17>
 F/788-819/Domain: EGF homology <EG18>
 F/826-857/Domain: EGF homology <EG19>
 F/864-895/Domain: EGF homology <EG20>
 F/902-933/Domain: EGF homology <EG21>
 F/936-1064/Region: avidin-like
 F/23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-27
 5,451-466,468-477,484-495/Default bonds: #status predicted
 F/489-504,506-515,522-533,527-542,544-553,560-571,565-580,582-591,598-609,603-618,620-62
 08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Default

Query Match 5.8%; Score 140; DB 2; Length 1064;

Best Local Similarity 33.6%; Pred.No.0.56; 51; Indels 16; Gaps 4;

Matches 42; Conservative 16; Mismatches 51; Indels 16; Gaps 4;
 QY 276 CSLTGKMTNDLGSNMITIGAVNSRGEFTGYITAVTATSNIEKSPHAGTQNTI-----N 329
 DB 939 CDLEGMWNECDQYTI-TKISTGMMLGDYMT-----YNERALGYAAPTVVVGYSN 989
 QY 330 KKTQPTFGFTVMKKSSESTTVFTGQCFLDRNGKEVILKTMWLLRSSYNDIGDDMKATRVGI 389
 DB 990 NYDFPSFGFTVVRDNGQSTTSWTGQCHL-CDGESEVLYTTWINTNMVSTCQDIKSNMVQ 1048
 QY 390 NIFTR 394
 DB 1049 DKWIR 1053

Search completed: February 16, 2006, 17:05:47
 Job time : 42 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 16:58:02 ; Search time 231 Seconds

(without alignments)
1221.694 Million cell updates/sec

Title: US-10-618-570-2

Perfect score: 2059
Sequence: 1 MAQMDPFDQEDTDSCTES.....DKATRVGINIFRLRQKE 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1381	67.1	453	1 MSRE_BOVIN	P21758 bos taurus
2	1042.5	50.6	388	2 O60505_HUMAN	O60505 homo sapien
3	1042.5	50.6	451	1 MSRE_HUMAN	P21757 homo sapien
4	987.5	48.0	454	1 MSRE_RABIT	Q05585 oryctolagus
5	830	40.3	354	2 O8CED7_MOUSE	O8ced7 mus musculus
6	801	38.9	458	1 MSRE_MOUSE	P32024 mus musculus
7	675	32.8	152	1 AVID_CHICK	P02701 gallus galli
8	664	32.2	152	2 O98SH4_CHICK	O98sh4 gallus galli
9	491	32.8	150	1 AVR4_CHICK	P56734 gallus galli
10	483.5	23.5	122	2 O8AY76_MEUGA	O8ay76 meleagris g
11	461	22.4	150	1 AVR3_CHICK	P56733 gallus galli
12	461	22.4	150	1 AVR7_CHICK	P56736 gallus galli
13	452	22.0	150	1 AVR1_CHICK	O13153 gallus galli
14	451	21.9	150	1 AVR6_CHICK	P56735 gallus galli
15	436	21.2	150	1 AVR2_CHICK	P56732 gallus galli
16	233	11.3	95	2 P70111_MESAU	P70111 mesocricetu
17	219	10.6	499	2 O5RFW0_BRARE	O5rfw0 brachydanto
18	204	9.9	400	2 O6ZM47_HUMAN	O6zm47 homo sapien
19	204	9.9	495	2 O6ZM47_HUMAN	O6zm47 homo sapien
20	199.5	9.7	374	2 O9CUC3_MOUSE	O9cuc3 mus musculus
21	195.5	9.5	491	2 O91WD6_MOUSE	O91wd6 mus musculus
22	194.5	9.4	387	2 O8BZ22_MOUSE	O8bz22 mus musculus
23	194.5	9.4	491	2 O8K299_MOUSE	O8k299 mus musculus
24	173.5	8.4	410	2 O4RF52_TETNG	O4rf52 tetradodon n
25	164.5	8.0	357	2 O7Z4A1_HUMAN	O7z4a1 homo sapien
26	163.5	7.9	280	2 O9D4G8_MOUSE	O9d4g8 mus musculus
27	144	7.0	283	2 O8R330_MOUSE	O8r330 mus musculus
28	144	7.0	283	2 O8R330_MOUSE	O8r330 mus musculus
29	141.5	6.9	778	2 O519A0_ENTHI	O519a0 entameoba h
30	141	6.8	980	2 O96WJ2_KULOLA	O96wj2 kluyveriomyc
31	140	6.8	1064	2 O73ML2_TREDE	O73ml2 treponema d
32	140	6.8	1064	1 FBPI_STRPU	P10079 strongyloce

32	139.5	6.8	183	1 SAV2_STRVL	O53533 streptomyce
33	138.5	6.7	183	1 SAV1_STRVL	O53532 streptomyce
34	138.5	6.7	183	1 SAV_STRVL	P22629 streptomyce
35	138.5	6.7	947	2 O61F09_PLAF7	O61f09 plasmodium
36	136	6.6	529	2 O25058_HELD	O25058 helioicidari
37	135.5	6.6	9439	2 O8CP76_STAEQ	O8cp76 staphylococ
38	135.5	6.6	10203	2 O5HPA2_STAEQ	O5hpa2 staphylococ
39	133.5	6.5	715	2 O51542_BORBU	O51542 borrelia bu
40	133.5	6.4	466	2 O8R3P2_MOUSE	O8r3p2 mus musculus
41	132.5	6.4	543	2 O8BMK4_MOUSE	O8bmk4 mus musculus
42	132.5	6.4	570	2 O97FD7_CIOAB	O97fd7 clostridium
43	132.5	6.4	1163	1 SBCC_CIOAB	O97fx1 clostridium
44	132	6.4	657	2 O4S759_TETNG	O4s759 tetradodon n
45	132	6.4	1461	2 O6KHX4_MYCWO	O6khx4 mycoplasma

ALIGNMENTS

RESULT 1

ID MSRE_BOVIN STANDARD; PRT; 453 AA.

AC P21758; 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Macrophage scavenger receptor types I and II (Macrophage acetylated

LDL receptor I and II).

GN Name=MSRL;

OC Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

OC Pecora; Bovidae; Bovinae; Bos.

OC NCBI_Taxid=9913;

OC [1]

NCBI_Taxid=9913;

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DR EMBL; X51689; CAA35987.1; -; mRNA.
DR *EMBL; X54183; CAA38108.1; -; mRNA.
DR PIR; S08276; S08276.
DR PIR; S08278; S08278.
DR InterPro; IPR008161; C1g_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR003543; Macscav_receptor.
DR InterPro; IPR001190; Srcr_receptor.
DR PANTHER; PTHR19311:SP5; Macscav_receptor; 1.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF03523; Macscav_rec; 1.
DR Pfam; PF00530; SRCR; 1.
DR PRINTS; PR01408; MACSCAVRCPTR.
DR PRINTS; PR0258; SPERACTRCPTR.
DR *ProDom; PD000007; C1g_helix; 1.
DR SMART; SM00202; SR; 1.
DR PROSITE; PS00420; SRCR_1; 1.
DR PROSITE; PS50287; SRCR_2; 1.
DR *Alternative splicing; Coiled coil; Collagen;
DR *Alternative splicing; Endocytosis; Glycoprotein; LDL; Receptor;
KW Signal-anchor; Transmembrane.
FT TOPO_DOM 1 50 Cytoplasmic (Potential).
FT TRANSMEM 1 76 Signal-anchor for type II membrane
FT FT protein (Potential).
FT TOPO_DOM 77 453 Extracellular (Potential).
FT DOMAIN 272 343 Collagen-like.
FT REGION 77 108 SRCR.
FT COILED 194 255 Spacer (Probable).
FT CARBOHYD 82 82 Potential.
FT CARBOHYD 101 101 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 142 142 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 183 183 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 220 220 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 248 248 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 266 266 N-linked (GlcNAc... ) (Potential).
FT DISULFID 377 441 By similarity.
FT DISULFID 390 451 By similarity.
FT DISULFID 421 431 By similarity.
FT VASPLIC 348 349 OS -> PG (in isoform II).
FT VASPLIC 350 453 /FTid=VSP_006227.
FT VASPLIC 350 453 Missing (in isoform II).
FT VASPLIC 350 453 /FTid=VSP_006228.
SQ SEQUENCE 453 AA; 50057 MW; 77A0FEFE48B00A21 CRC64;

Query Match 67.1%; Score 1381; DB 1; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.2e-75;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AC O60505;
DT 01-AUG-1998 (TRENBLUREL. 07, Created)
DT 01-AUG-1998 (TRENBLUREL. 07, Last sequence update)
DT 01-MAR-2004 (TRENBLUREL. 26, Last annotation update)
DE Macrophage scavenger receptor type III.
GN Name=SR-A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo
OC NCBI_TaxID=9606;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=98208366; PubMed=9548586;
RA Gough P.J., Greaves D.R., Gordon S.;
RT "A naturally occurring isoform of the human macrophage scavenger
RT receptor (SR-A) gene generated by alternative splicing blocks modified
RT LDL uptake."
RT J. Lipid Res. 39:531-543(1998).
DR EMBL; AF037351; AAC09251.1; -; mRNA.
DR HSSP; Q08380; 1BY2.
DR Ensembl; ENSG0000003945; Homo sapiens.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR GO; GO:0006898; P:receptor mediated endocytosis; IEA.
DR InterPro; IPR008161; C1g_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR003543; Macscav_receptor.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF03523; Macscav_rec; 1.
DR Pfam; PF00530; SRCR; 1.
DR PRINTS; PR01408; MACSCAVRCPTR.
DR PRINTS; PR0258; SPERACTRCPTR.
DR ProDom; PD000007; C1g_helix; 1.
DR SMART; SM00202; SR; 1.
DR PROSITE; PS50287; SRCR_2; 1.
KW Collagen; Receptor.
SQ SEQUENCE 388 AA; 42942 MW; D6A20BC857BFB46 CRC64;

Query Match 50.6%; Score 1042.5; DB 2; Length 388;
Best Local Similarity 72.2%; Pred. No. 5.3e-55;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;
```

DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Macrophage scavenger receptor types I and II (Macrophage acetylated
 DE LDL receptor I and II) (CD204 antigen).
 GN Name=MSR1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORMS I AND II).
 RX MEDLINE=91067661; PubMed=2251254;
 RA Matsunoto A., Naito M., Itakura H., Ikemoto S., Asaoka H.,
 RA Hayakawa I., Kanamori H., Aburatani H., Takaku F., Suzuki H.,
 RA Kobayashi Y., Miyai T., Takahashi K., Cohen E.H., Wydro R., Houseman D.E.,
 RA Kodama T.,
 RT "Human macrophage scavenger receptors: primary structure, expression,
 RT and localization in atherosclerotic lesions".
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9133-9137(1990).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM I).
 RC TISSUE=Testis;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditschenko L., Marusina K., Farmer A.M., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein W.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
 RA Butcherfield J.S.N., Krzywicki M.I., Skalka A., Smalls D.E.,
 RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE OF 155-272.
 RX PubMed=8093617;
 RA Emi M., Asaoka H., Matsumoto A., Itakura H., Kurihara Y., Wada Y.,
 RA Kanamori H., Yataki Y., Takahashi B., Lepetit M.,
 RT "Structure, organization, and chromosomal mapping of the human
 RT macrophage scavenger receptor gene".
 RL J. Biol. Chem. 268:2120-2125(1993).
 RN [4]
 RP SRCR DOMAIN DISULFIDE BONDS.
 RX MEDLINE=97059147; PubMed=8900177; DOI=10.1074/jbc.271.43.26924;
 RA Reenlik D., Chatterton J.B., Schwartz K., Slayter H., Krieger M.,
 RT "Structures of class A macrophage scavenger receptors. Electron
 RT microscopic study of flexible, multidomain, fibrous proteins and
 RT determination of the disulfide bond pattern of the scavenger receptor
 RT cysteine-rich domain".
 RL J. Biol. Chem. 271:26924-26930(1996).
 RN [5]
 RP SPICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
 RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-28;
 RA Hallman R.T., Green R.E., Brenner S.E.,
 RT "An unappreciated role for RNA surveillance".
 CC Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
 CC *-1- FUNCTION: Membrane glycoprotein implicated in the pathologic
 CC deposition of cholesterol in arterial walls during atherogenesis.
 CC Two types of receptor subunits exist. These receptors mediate the
 CC endocytosis of a diverse group of macromolecules, including
 CC modified low density lipoproteins (LDL).
 CC *-1- SUBUNIT: Homotrimer.

[illegible]

Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQNDPDPQEDDTSCTESYKFPDARSVTALLPBPKNKGPPTLQERMSYKATLITLYIV 60
 DB 1 MEQNDHFNQDQEDDTSCTESYKFPDARSVTALLPBPKNKGPPTLQERMSYKATLITLYIV 60
 QY 61 FVLVPIPIIGVAAQLKMKETKNCVGSVNA-DISPSPGKNGSEDEMRFREAVEMRSN 119
 DB 61 FAVLIPILIGVAAQLKMKETKNCVGSVNA-DISPSPGKNGSEDEMRFREAVEMRSN 120
 QY 120 MESRIQVLSDEANILDAKNFONFSITTDQRFNVFLFOLNSLSSIOGHENITGDISKS 179
 DB 121 MEKRIQVLSDEANILDAKNFONFSITTDQRFNVFLFOLNSLSSIOGHENITGDISKS 180
 QY 180 VGLNTTVLDLQFSTETLNGRVOENAFKQOEERKLEERINYASAEIKSLDEKQVYLEOEI 239
 DB 181 ISLNTTLLDLHLVETLNKQVETLKGQEBISKLKEERVYNASAEIKSLDEKQVYLEOEI 240
 QY 240 KGEKMLNNTNDRLKDMWHSQTLRNITLLQG 272
 DB 241 KGEVVLNNTNDRLKDMWHSQTLRNITLLQG 273

RESULT 4
 MSRE_RABIT STANDARD; PRT; 454 AA.
 ID MSRE_RABIT 005585;
 AC 005585;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Macrophage scavenger receptor types I and II (Macrophage acetylated LDL receptor I and II).
 DE LDL receptor I and II).
 GN Name=MSR1;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93016877; PubMed=1401078;
 RA Bickel P.B., Freeman M.W.;
 RT "Rabbit aortic smooth muscle cells express inducible macrophage scavenger receptor messenger RNA that is absent from endothelial cells";
 RT J. Clin. Invest. 90:1450-1457(1992).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93131972; PubMed=8380589;
 RA Doi T., Wada Y., Kodama T., Higashi K.I., Kurihara Y., Miyazaki T., Nakamura H., Ueugli S., Imanishi T., Kawabe Y., Itakura H., Yazaki Y., Matsunoto A.;
 RT "Charged collagen structure mediates the recognition of negatively charged macromolecules by macrophage scavenger receptors";
 RT J. Biol. Chem. 268:2126-2133(1993).
 CC -1- FUNCTION: Membrane glycoproteins implicated in the pathologic deposition of cholesterol in arterial walls during atherosclerosis. Two types of receptor subunits exist. These receptors mediate the endocytosis of a diverse group of macromolecules, including modified low density lipoproteins (LDL).
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=I;
 CC IsoId=Q05585-1; Sequence=Displayed;
 CC Name=II;
 CC IsoId=Q05585-2; Sequence=VSP_006233, VSP_006234;
 CC -1- SIMILARITY: Contains 1 collagen-like domain.
 CC -1- SIMILARITY: Contains 1 SRCR domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration -
 CC the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC EMBL; L11693; AAA31402.1; -; mRNA.
 CC EMBL; L11692; AAA31403.1; -; mRNA.
 CC EMBL; D13381; BA02649.1; -; mRNA.
 CC PIR; I46862; I46862.
 CC PIR; I46863; I46863.
 CC InterPro; IPR008161; C1g helix.
 CC InterPro; IPR008160; Collagen.
 CC InterPro; IPR003543; Macscav_receptor.
 CC InterPro; IPR001190; Src_receptor.
 CC PANTHER; PTHR19331; SF5; Macscav_receptor; 1.
 CC Pfam; PF01391; Collagen; 1.
 CC Pfam; PF03523; Macscav_rec; 1.
 CC Pfam; PF00530; SRCR; 1.
 CC PRINTS; PR01408; MACSCAVRCPT.
 CC PRINTS; PR00258; SPERACTRCPT.
 CC ProDom; PD000007; C1g helix; 1.
 CC SMART; SM00420; SRCR_1; 1.
 CC PROSITE; PS00287; SRCR_2; 1.
 CC PROSITE; PS00287; SRCR_2; 1.
 CC KW Alternative splicing; Coiled
 KW Glycoprotein; LDL; Receptor;
 FT TOPO_DOM 1 50
 FT TRANSMEM 51 73
 FT TOPO_DOM 74 454
 FT DOMAIN 273 344
 FT DOMAIN 353 453
 FT REGION 74 109
 FT COILED 199 256
 FT CARBOHYD 82 82
 FT CARBOHYD 102 102
 FT CARBOHYD 143 143
 FT CARBOHYD 184 184
 FT CARBOHYD 221 221
 FT CARBOHYD 249 249
 FT CARBOHYD 267 267
 FT DISULFID 378 442
 FT DISULFID 391 452
 FT DISULFID 422 432
 FT VARSPLD 348 354
 FT VARSPLIC 355 454
 FT CONFLICT 106 106
 FT SEQUENCE 454 AA; 49745 MW; 527A79692EA76429 CRC64;
 SQ

Query Match 48.0%; Score 987.5; DB 1; Length 454;
 Best Local Similarity 68.9%; Pred. No. 1.4e-51;
 Matches 188; Conservative 44; Mismatches 40; Indels 1; Gaps 1;

QY 1 MAQNDPDPQEDDTSCTESYKFPDARSVTALLPBPKNKGPPTLQERMSYKATLITLYIV 60
 DB 1 MAQNDPDPQEDDTSCTESYKFPDARSVTALLPBPKNKGPPTLQERMSYKATLITLYIV 60
 QY 61 FVLVPIPIIGVAAQLKMKETKNCVGSVNA-DISPSPGKNGSEDEMRFREAVEMRSN 119
 DB 61 FAVLIPILIGVAAQLKMKETKNCVGSVNA-DISPSPGKNGSEDEMRFREAVEMRSN 120
 QY 120 MESRIQVLSDEANILDAKNFONFSITTDQRFNVFLFOLNSLSSIOGHENITGDISKS 179
 DB 121 MEKRIQVLSDEANILDAKNFONFSITTDQRFNVFLFOLNSLSSIOGHENITGDISKS 180
 QY 180 VGLNTTVLDLQFSTETLNGRVOENAFKQOEERKLEERINYASAEIKSLDEKQVYLEOEI 239
 DB 181 ISLNTTLLDLHLVETLNKQVETLKGQEBISKLKEERVYNASAEIKSLDEKQVYLEOEI 240
 QY 240 KGEKMLNNTNDRLKDMWHSQTLRNITLLQG 272
 DB 241 KGEVVLNNTNDRLKDMWHSQTLRNITLLQG 273

RESULT 5
 Q8CED7_MOUSE PRELIMINARY; PRT; 354 AA.
 AC Q8CED7_MOUSE PRELIMINARY; PRT; 354 AA.
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 26, Last annotation update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched
 DE library, clone:461424C05 product:macrophage scavenger receptor 1,
 DE full insert sequence.
 GN Name=Msr1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsumoto Y., Nishikawa I., Resole G., Quackenbush J.,
 RA Schiml L.M., Stambli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,
 RA Brownstein W.O., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guelinich S., Hill D., Hofmann M., Hume D.A., Kamitani M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilmshurst L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RA The PANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Saeki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwa K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-Format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RA Adachi J., Aizawa K., Akiyama T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Horii F., Imoto K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kuribara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyokawa K., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK028480; BAC25973.1; -, mRNA.
 DR MGI; MGI:98257; Msr1.
 DR GO; GO:0005737; Cytoplasm; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0005044; F:scavenger receptor activity; IEA.
 DR GO; GO:0006817; P:phosphate transport; IEA.
 DR GO; GO:0006898; P:receptor mediated endocytosis; IEA.
 DR InterPro; IPR008161; C1g_helix.
 DR InterPro; IPR008160; C1g_helix.
 DR InterPro; IPR00543; Maccscv_receptor.
 DR InterPro; IPR002017; Spectrin.
 DR Pfam; PF01391; Collagen; 1.
 DR Pfam; PF03523; Maccscv_rec; 1.
 DR PRINTS; PR01408; MACSCVRCPT.
 DR Prodom; PD000007; C1g_helix; 1.
 KW Receptor.
 SQ SEQUENCE 354 AA; 38773 MW; 348E084D2D8B644B CRC64;
 Query Match 40.3%; Score 830; DB 2; Length 354;
 Best Local Similarity 60.9%; Pred. No. 3,4e-42;
 Matches 162; Conservative 47; Mismatches 55; Indels 2; Gaps 2;
 QY 8 PPOQEDTSCISYKVPDASVTALLPPIPKXGPTIOERKSKYKTLITLVFVVI 67
 DB 13 PHEQBDACSSSESVKFDASMTASLPSTKXNPSLOEKSKFKAALIALYLVFVLPV
 QY 68 IGIYVAQLLKMETKCTGVSVN-ADISPEEGKNGSEDEMFREAVNMRMSRITQY 126
 DB 73 VGIVTRQQLINWEMKICVLSINTSOTSGPKMKENTSKYEMFP-TIIEHMDMERIES 131
 QY 127 LSDNEANLDAKNFONFSITTDQFNDVLFQNLISLSIOEHENITIGDISKVLGNTTV 186
 DB 132 ISNSKADILDTFRFQNFMSWATDQRLNDILQLNSLISSVQEHGNSLDLMSKLSQSLNMTL 191
 QY 187 LDLOFSIFTLNKGROENAFKQOEEMRKLEERLYNSAETKSLDEQVYVLEOIKEMKLL 246
 DB 192 LDVQHTETLTNVRVSESTAKQOEDISKLEERVYKVAEVSQAEQAHVEQVKEQVRLV 251
 QY 247 NNITNDLRKLKDWESQTLKNITLLOG 272
 DB 252 NNITNDLRKLKDWESQTLKNITFIQ 277
 RESULT 6
 MSRE_MOUSE
 ID MSRE_MOUSE STANDARD; PRT; 458 AA.
 AC P30204; O923G0; Q90Z56;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Macrophage scavenger receptor types I and II (Macrophage acetylated
LDL receptor I and II) (Scavenger receptor type A) (SR-A).
GN Name=Msr1; Synonyms=Scvr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS I AND II).
RX MEDLINE=93359822; PubMed=8394668;
RA Ashkenas J., Penman M., Vasilis E., Acton S., Freeman M.W., Krieger M.,
RT "Structures and high and low affinity ligand binding properties of
murine type I and type II macrophage scavenger receptors.";
RL J. Lipid Res. 34:983-1000(1993).
[2]
RP NUCLEOTIDE SEQUENCE (ISOFORM II).
RX MEDLINE=93131972; PubMed=8380589;
RA Doi T., Wada Y., Kodama T., Higashi K.I., Kurihara Y., Miyazaki T.,
RA Nakamura H., Uesugi S., Imanishi T., Kawabe Y., Itakura H., Yazaki Y.,
RA Matsunoto A.;
RT "Charged collagen structure mediates the recognition of negatively
charged macromolecules by macrophage scavenger receptors.";
RL J. Biol. Chem. 268:2126-2133(1993).
[3]
RP NUCLEOTIDE SEQUENCE (ISOFORM I).
RX STRAIN=C57BL/6;
RA Rateri D.L., Whitman S.C., Block A.E., Daugherty A.;
RT "Identification of a functional domain in class A scavenger receptors
that mediates metabolism of acLDL.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[4]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM II).
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,
RA Nishida I., Osato N., Saito R., Suzuki H., Yamashita I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balderas R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schmitt L.M., Kanapin A., Matsuda H., Batalov S., Beisler K.W.,
RA Blake J.A., Brad D., Brusic V., Chochia S., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanagaya A., Kurichkin I.V., Lee Y., Lemhard B., Lyons P.A.,
RA MacIot D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Savelkin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vetraro R., Wagner L., Wahlestedt C., Wang Y., Waranabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Borje A., Yangisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carlini P., Hayatsu N.,
RA Hitzonen-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda I.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yamashita A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[5]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM II).
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schenker C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Cabavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Logueller N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
RP NUCLEOTIDE SEQUENCE OF 349-458.
RX MEDLINE=91062370; PubMed=1978939;
RA Freeman M., Ashkenas J., Rees D.J., Kingsley D.M., Copeland N.G.,
RA Jenkins N.A., Krieger M.;
RT "An ancient, highly conserved family of cysteine-rich protein domains
revealed by cloning type I and type II murine macrophage scavenger
receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8810-8814(1990).
[7]
RP NUCLEOTIDE SEQUENCE OF 1-4.
RX MEDLINE=95395388; PubMed=7666008;
RA Aftiring R.P., Freeman M.W.;
RT "Structure of the murine macrophage scavenger receptor gene and
evaluation of sequences that regulate expression in the macrophage
cell line, P388D.";
RL J. Lipid Res. 36:1305-1314(1995).
CC -1- FUNCTION: Membrane glycoproteins implicated in the pathologic
deposition of cholesterol in arterial walls during atherosclerosis.
CC Two types of receptor subunits exist. These receptors mediate the
endocytosis of a diverse group of macromolecules, including
modified low density lipoproteins (LDL).
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=I;
CC IsoId=P30204-1; Sequence=Displayed;
CC Name=II;
CC IsoId=P30204-2; Sequence=VSP_006231, VSP_006232;
CC -1- SIMILARITY: Contains 1 collagen-like domain.
CC -1- SIMILARITY: Contains 1 SRCR domain.
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the European Bioinformatics Institute. There are no restrictions on its
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removed.

EMBL, L04274; AAA39747.1; ALT_INIT; mRNA.
EMBL, L04275; AAA39748.1; ALT_INIT; mRNA.
EMBL, D13382; BAA02650.1; -; mRNA.
EMBL, AF203781; AAF14001.1; -; mRNA.
EMBL, M59445; AAA37464.1; -; mRNA.
EMBL, M59446; AAA37465.1; -; mRNA.
EMBL, U13673; AAC13774.1; -; Genomic DNA.
EMBL, AK089178; BAC40779.1; -; Genomic DNA.
EMBL, BC003814; AA03814.1; -; mRNA.
PIR, B44407; B44407.
DR Ensembl: ENSMUSG00000025044; Mus musculus.
DR MGI: 98257; Msr1.
DR GO: 0016021; C:Integral to membrane; TAS.
DR InterPro: IPR008160; C1g_helix.
DR InterPro: IPR003543; Macscav_receptor.
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR001190; Srcr_receptor.
DR PANTHER: PTHR19331:SF5; Macscav_receptor; 1.
DR Pfam: PF01391; Collagen; 1.

DR Pfam: PF03523; Macscav_rec; 1.
 DR Pfam: PF00530; SRCR; 1.
 DR PRINTS; PR01408; MACSCAVRCPR.
 DR PRINTS; PR00258; SPERACTRCPR.
 DR PRODOM; PD000007; C1g_helix; 1.
 DR PROSITE; PS00420; SRCR_1; 1.
 DR PROSITE; PS00287; SRCR_2; 1.
 KW Alternative splicing; Coiled coil; Collagen; Endocytosis;
 KW Glycoprotein; LDL Receptor; Signal-anchor; Transmembrane;
 KW Topo_dom
 FT TOPO_DOM 1 55
 FT TRANSMEM 56 78
 FT TOPO_DOM 79 458
 FT DOMAIN 277 350
 FT REGION 357 457
 FT COILED 79 114
 FT CARBOHYD 299 259
 FT CARBOHYD 94 94
 FT CARBOHYD 107 107
 FT CARBOHYD 147 147
 FT CARBOHYD 168 188
 FT CARBOHYD 253 253
 FT CARBOHYD 271 271
 FT DISULFID 382 446
 FT DISULFID 395 456
 FT DISULFID 426 436
 FT VARSPPLIC 352 354
 FT VARSPPLIC 355 458
 FT CONFLICT 47 47
 FT CONFLICT 110 110
 FT CONFLICT 120 120
 FT CONFLICT 130 130
 FT CONFLICT 168 168
 FT CONFLICT 202 202
 SQ SEQUENCE 458 AA; 50131 MW; 6DAC041C27EE50B CRC64;
 Query Match 38.9%; Score 801; DB 1; Length 458;
 Best Local Similarity 59.4%; Pred. No. 2.6e-40;
 Matches 158; Conservative 46; Mismatches 60; Indels 2; Gaps 2;

QY 8 PPOQBDTSCTSEKVFDAKSTVALLPPHPKNGPTLOERKSKYKALITLYLVFVLPVI 67
 DB 13 PHEREDADSSSVKFDARSMTHSLPHSTRKGPVSQEKSKKALIALIYLVFAVLIV 72
 QY 68 IGIYVAQLKWKETKQCTVGSVN-ADISPEEGKNGSEDEMRPREAVMERMSNRIOY 126
 DB 73 VGIYVAQLKWKEMKQCLVCSRYMTSPTSQGPMEKENTSNVEMPF-TIIMAHMDMERIOG 131
 QY 127 LSDNEANLIDAKNFQNFSTITTPORRNDVLPOLNSLSSIOEHENIIGDISKLVGLNTTV 186
 DB 132 ISNSKADILDTGRFONFMSWATDORLNDILLQNSLITLSVQEHGNSIDALSKLSQSLNMTL 191
 QY 187 LDLOSIETITNGRVONENAFKQOEEMRKLEERLYNSAKIKSDEKOVYLEOIKGSMKLL 246
 DB 192 LDVQLHTETLHVRVVESTAKQOEDISKLEERYKYSAEQVKEQDAHVEQVQKVRVL 251
 QY 247 NNITNDLRKDWESQTLKNITLQO 272
 DB 252 NNITNDLRKDWESQTLKNITFIQO 277

RESULT 7
 AVID CHICK STANDARD; PRT; 152 AA.
 AC P02701; Q91958;
 DT *21-JUL-1986 (Rel. 01. Created)
 DT 01-NOV-1991 (Rel. 20. Last sequence update)
 DT 13-SEP-2005 (Rel. 48. Last annotation update)
 DE Avidin precursor.
 GN Name=AVID;
 OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus
 OK NCBI_Taxid=9031;
 RN (1)
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=87203384; PubMed=3575102;
 RA Gope M.L., Keinänen R.A., Kristo P.A., Connely O.M., Beattie W.G.,
 RA Zarucki-Schultz T., O'Malley B.W., Kulomaa M.S.;
 RT "Molecular cloning of the chicken avidin cDNA."
 RL Nucleic Acids Res. 15:3595-3606(1987).
 RN (2)
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=90355928; PubMed=2143802; DOI=10.1016/0076-6879(90)84261-E;
 RA Chandra G., Gray J.G.;
 RT "Cloning and expression of avidin in Escherichia coli."
 RL Meth. Enzymol. 184:70-79(1990).
 RN (3)
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=white leghorn; TISSUE=oviduct;
 RX MEDLINE=95394357; PubMed=7665080; DOI=10.1016/0378-1119(95)00187-B;
 RA Wallen M.J., Laukkanen M.O., Kulomaa M.S.;
 RT "Cloning and sequencing of the chicken egg-white avidin-encoding gene
 and its relationship with the avidin-related genes Avr1-Avr5."
 RL Gene 161:205-209(1995).
 RN (4)
 RN PROTEIN SEQUENCE OF 25-152. AND CARBOHYDRATE-LINKAGE SITE ASN-41.
 RX MEDLINE=71107558; PubMed=5100763;
 RA Delange R.J., Huang T.-S.;
 RT "Egg white avidin. 3. Sequence of the 78-residue middle cyanogen
 bromide peptide. Complete amino acid sequence of the protein
 subunit."
 RL J. Biol. Chem. 246:698-709(1971).
 RN (5)
 RN PROTEIN SEQUENCE OF 25-152. AND VARIANT THR-58.
 RX MEDLINE=71107557; PubMed=5100762;
 RA Huang T.-S., Delange R.J.;
 RT "Egg white avidin. II. Isolation, composition, and amino acid
 sequences of the tryptic peptides."
 RL J. Biol. Chem. 246:686-697(1971).
 RN (6)
 RN IMPORTANCE OF TYR IN BIOTIN-BINDING.
 RX MEDLINE=90351377; PubMed=2386489;
 RA Gitlin G., Bayer E.A., Wilchek M.;
 RT "Studies on the biotin-binding sites of avidin and streptavidin.
 Tyrosine residues are involved in the binding site."
 RL Biochem. J. 269:527-530(1990).
 RN (7)
 RN BIOTIN-BINDING STUDIES.
 RX MEDLINE=91378911; PubMed=1898347;
 RA Hiller Y., Bayer E.A., Wilchek M.;
 RT "Studies on the biotin-binding site of avidin. Minimized fragments
 that bind biotin."
 RL Biochem. J. 278:573-585(1991).
 RN (8)
 RN STRUCTURE OF CARBOHYDRATE.
 RX MEDLINE=83075332; PubMed=6816268;
 RA Bruch R.C., White H.B. III;
 RT "Compositional and structural heterogeneity of avidin glycopeptides."
 RL Biochemistry 21:5334-5341(1982).
 RN (9)
 RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=93281699; PubMed=8506353;
 RA Livnah O., Bayer E.A., Wilchek M., Sussman J.L.;
 RT "Three-dimensional structures of avidin and the avidin-biotin
 complex."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5076-5080(1993).
 RN (10)
 RN X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=93294833; PubMed=8515446;
 RA Pugliese L., Coda A., Malcovati M., Bolognesi M.;
 RT "Three-dimensional structure of the tetragonal crystal form of egg-
 white avidin in its functional complex with biotin at 2.7-A

RT resolution." ;
 RL "J. Mol. Biol. 231:698-710(1993).
 [11]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=94430987; PubMed=9760187;
 RA Nadone E., Rosano C., Santambrogio P., Curnis F., Corti A., Magni F.,
 RA Slocardi A.G., Paganelli G., Losso R., Aprea B., Bolognesi M.,
 RA Sidioli A., Arosio P.;
 RT "Biochemical characterization and crystal structure of a recombinant
 hen avidin and its acidic mutant expressed in Escherichia coli." ;
 RL Eur. J. Biochem. 256:453-460(1998).
 CC -1- FUNCTION: The biological function of avidin is not known. Forms a
 strong non-covalent specific complex with biotin (one molecule of
 biotin per subunit of avidin).
 CC -1- SUBUNIT: Homotrimer.
 CC -1- TISSUE SPECIFICITY: Synthesized in hen oviduct and concentrated in
 egg white (where it represent 0.05% of the total protein).
 CC -1- PTM: N-linked glycan at Asn-41 consists of GlcNAc(beta1-2)
 2)Man(alpha1-3)[GlcNAc(beta1-4)]Man(alpha1-6)]
 CC Man(beta1-4)GlcNAc(beta1-4)GlcNAc.
 CC -1- SIMILARITY: Belongs to the avidin/streptavidin family.
 CC -1- DATABASE: NAME=Washington enzyme manual;
 WWW="http://www.worthington-biochem.com/AV/".
 CC -----
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 DR EMBL; X05343; CAA28954.1; -; mRNA.
 DR EMBL; L27818; AAB59733.1; -; Genomic DNA.
 DR PIR; A54975; VICH.
 DR PDB; 1AVD; X-ray; A/B=25-152.
 DR PDB; 1AVB; X-ray; A/B=25-152.
 DR PDB; 1JUG; X-ray; A/B=25-152.
 DR PDB; 1LDO; X-ray; A/B=25-152.
 DR PDB; 1LDO; X-ray; A/B=25-152.
 DR PDB; 1LEL; X-ray; A/B=25-152.
 DR PDB; 1NQN; X-ray; A/B=25-147.
 DR PDB; 1RAV; X-ray; A/B=26-152.
 DR PDB; 2AVI; X-ray; A/B=25-152.
 DR PDB; 2CAM; X-ray; A/B=28-152.
 DR GLYCOBASE; P02701; -.
 DR Ensembl; ENSGALG0000002446; Gallus gallus.
 DR InterPro; IPR005469; Avidin.
 DR InterPro; IPR005468; Avidin/str.
 DR Pfam; PF01382; Avidin; 1.
 DR PRINTS; PR00709; AVIDIN.
 DR PROSITE; PS00577; AVIDIN; 1.
 KW 3D-structure; Biotin; Direct protein sequencing; Glycoprotein;
 KW Polymorphism; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 152 Avidin.
 FT BINDING 57 57 Biotin.
 FT CARBOHYD 41 41 N-linked (GlcNAc...).
 FT FTID=CAR_000230.
 FT DISULFID 28 107 I -> T (in about 50% of the chains).
 FT VARIANT 58 58 G -> S (in Ref. 3).
 FT CONFLICT 22 22 E -> Q (in Ref. 2 and 3).
 FT STRAND 32 36
 FT TURN 37 38
 FT STRAND 41 44
 FT TURN 49 50
 FT STRAND 52 60
 FT STRAND 68 77
 FT HELIX 80 82
 FT STRAND 87 93
 FT TURN 100 109
 FT STRAND 111 112
 FT STRAND 115 124
 FT HELIX 130 135

FT STRAND 137 146
 SQ SEQUENCE 152 AA; 16769 MW; 1D55A4491D5EFDEC CRC64;
 Query Match 32.8%; Score 675; DB 1; Length 152;
 Best Local Similarity 99.2%; Pred. No. 2.8e-33;
 Matches 127; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 273 ARKSLGKMTNDGSGNMVTIGAVNSRGEFTGTITAVATSNELKESPLHGTONTINKRT 332
 DB 25 ARKSLGKMTNDGSGNMVTIGAVNSRGEFTGTITAVATSNELKESPLHGTONTINKRT 84
 QY 333 QPTGFVNMKFSSTVFTGQCIDRNGKVLKTMILRSSVNDIGDMATRVGINIF 392
 DB 85 QPTGFVNMKFSSTVFTGQCIDRNGKVLKTMILRSSVNDIGDMATRVGINIF 144
 QY 393 TRLRTOKE 400
 DB 145 TRLRTOKE 152
 RESULT 8
 ID Q98SH4_CHICK PRELIMINARY; PRT; 152 AA.
 AC Q98SH4;
 DT 01-JUN-2001 (TRENBLREL, 17, Created)
 DT 01-JUN-2001 (TRENBLREL, 17, Last sequence update)
 DT 01-OCT-2002 (TRENBLREL, 22, Last annotation update)
 DE Avidin precursor.
 GN Name=AVD;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Metazoa; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=95394357; PubMed=7665080; DOI=10.1016/0378-1119(95)00187-B;
 RA Wallen M.J., Laakkonen M.O., Kulomaa M.S.;
 RT "Cloning and sequencing of the chicken egg-white avidin-encoding gene
 and its relationship with the avidin-related genes Avrl-Avrs." ;
 RL Gene 161:205-209(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21070478; PubMed=1167523;
 RA Ahlroth M.K., Kola E.H., Ewald D., Masabanda J., Sazanov A., Fries R.,
 RA Kulomaa M.S.;
 RT "Characterization and chromosomal localization of the chicken avidin
 gene family." ;
 RL Anim. Genet. 31:367-375(2000).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Ahlroth M.K.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ311647; CAC34569.1; -; Genomic DNA.
 DR HSSP; P02701; 1108.
 DR SMR; Q98SH4; 26-149.
 DR Ensembl; ENSGALG0000002446; Gallus gallus.
 DR InterPro; IPR005469; Avidin.
 DR InterPro; IPR005468; Avidin/str.
 DR Pfam; PF01382; Avidin; 1.
 DR PRINTS; PR00709; AVIDIN.
 DR PROSITE; PS00577; AVIDIN; 1.
 KW Signal.
 FT SIGNAL 1 24 Potential.
 FT SEQUENCE 152 AA; 16742 MW; 04B49658670B974B CRC64;
 Query Match 32.2%; Score 664; DB 2; Length 152;
 Best Local Similarity 97.7%; Pred. No. 1.3e-32;
 Matches 125; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 273 ARKSLGKMTNDGSGNMVTIGAVNSRGEFTGTITAVATSNELKESPLHGTONTINKRT 332
 DB 25 ARKSLGKMTNDGSGNMVTIGAVNSRGEFTGTITAVATSNELKESPLHGTONTINKRT 84

QY 333 OPTFGFTVWKKFSESTTVFTGQCFIDRNGEVLKTMMLLRSSVNDIGDWMKATRVGINIF 392
DB 85 OPTFGFTVWKKFSESTTVFTGQCFIDRNGEVLKTMMLLRSSVNDIGDWMKATRVGINIF 144

QY 393 TRLRTOKE 400
DB 145 TRLRTOKE 152

RESULT 9
AVR4_CHICK STANDARD; PRT; 150 AA.
ID AVR4_CHICK
AC P56734;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Avidin-related protein 4/5 precursor.
GN Name=AVR4;
GN and
GN Name=AVR5;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CC NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=White leghorn; TISSUE=Oviduct;
RX MEDLINE=94170814; PubMed=8125122;
RA Keinaenen R.A., Wallen M.J., Kristo P.A., Laukkanen M.O.,
RA Toimela T.A., Helenus M.A., Kulmaa M.S.;
RT "Molecular cloning and nucleotide sequence of chicken avidin-related
RT genes 1-5."
RL Eur. J. Biochem. 220:615-621(1994).
CC -1- MISCELLANEOUS: The sequences of the coding regions of genes AVR4
CC and AVR5 are identical.
CC -1- SIMILARITY: Belongs to the avidin/streptavidin family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL, Z22883; -, NOT ANNOTATED_CDS; Genomic_DNA.
DR PIR, S42204;
DR PDB, 1Y52; X-ray; X/Y=25-150.
DR PDB, 1Y53; X-ray; X/Y=25-150.
DR PDB, 1Y55; X-ray; X/Y=25-150.
DR SMR, P56734; 26-147.
DR EMBL, ENSGALG0000002441; Gallus gallus.
DR InterPro, IPR005468; Avidin.
DR InterPro, IPR005468; Avidin.
DR Pfam, PF01382; Avidin; 1.
DR PRINTS, PR00709; Avidin.
DR PROSITE, PS00577; AVIDIN, 1.
KM 3D-structure; Biotin; Glycoprotein; Multigene family; Signal.
FT SIGNAL 1 24
FT CHAIN 25 150
FT BINDING 57 57
FT CARBOHYD 67 67
FT CARBOHYD 93 93
FT CARBOHYD 141 141
SQ SEQUENCE 150 AA; 16644 MW; 9A6C6C6310EF813A CRC64;

Query Match 23.8%; Score 491; DB 1; Length 150;
Best Local Similarity 76.6%; Pred. No. 3.7e-22;
Matches 98; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

QY 273 ARKCSLTGKWTNDLGSNMITGAVNSRGFTGTYTAVTATSNIEKSPHLGTONTINKRT 332
DB 25 ARKCSLTGKWTNDLGSNMITGAVNSRGFTGTYTAVTATSNIEKSPHLGTONTINKRT 82

QY 333 OPTFGFTVWKKFSESTTVFTGQCFIDRNGEVLKTMMLLRSSVNDIGDWMKATRVGINIF 392
DB 83 OPTFGFTVWKKFSESTTVFTGQCFIDRNGEVLKTMMLLRSSVNDIGDWMKATRVGINIF 142

QY 393 TRLRTOKE 400
DB 143 TRLCTVEE 150

RESULT 10
OSAV76_MEIGA PRELIMINARY; PRT; 122 AA.
ID OSAV76_MEIGA
AC OSAV76;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Avidin (Fragment).
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
CC NCBI_TaxID=9103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22755852; PubMed=12672662; DOI=10.1095/biolreprod.102.015172;
RA Long E.L., Sonstegard T.S., Long J.A., Van Tassel C.P., Zuelke K.A.;
RT "Serial analysis of gene expression in turkey sperm storage tubules in
RT the presence and absence of resident sperm."
RT Biol. Reprod. 69:469-474(2003).
DR EMBL, AF545846; AAN38297.1; -, mRNA.
DR HSSP, P02701; 120N.
DR SMR, OSAV76; 25-122.
DR InterPro, IPR005469; Avidin.
DR InterPro, IPR005468; Avidin/str.
DR Pfam, PF01382; Avidin; 1.
DR PRINTS, PR00709; AVIDIN.
FT NON TER 122
SQ SEQUENCE 122 AA; 13368 MW; 3D22EE74480E97E0 CRC64;

Query Match 23.5%; Score 483.5; DB 2; Length 122;
Best Local Similarity 82.9%; Pred. No. 8.1e-22;
Matches 92; Conservative 8; Mismatches 8; Indels 3; Gaps 1;

QY 264 LKNTLTL---QGARCSLTGKWTNDLGSNMITGAVNSRGFTGTYTAVTATSNIEKSP 320
DB 12 LKNTLTLPGHSARKCLTGKWTNDLGSNMITGAVNSRGFTGTYTAVTATSNIEKSP 71

QY 321 LHGTONTINKRTQPTFGFTVWKKFSESTTVFTGQCFIDRNGEVLKTMML 371
DB 72 LHGTONTINKRTQPTFGFTVWKKFSESTTVFTGQCFIDRNGEVLKTMML 122

RESULT 11
AVR3_CHICK STANDARD; PRT; 150 AA.
ID AVR3_CHICK
AC P56733;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Avidin-related protein 3 precursor.
GN Name=AVR3;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CC NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=White leghorn; TISSUE=Oviduct;
RX MEDLINE=94170814; PubMed=8125122;
RA Keinaenen R.A., Wallen M.J., Kristo P.A., Laukkanen M.O.,
RA Toimela T.A., Helenus M.A., Kulmaa M.S.;
RT "Molecular cloning and nucleotide sequence of chicken avidin-related

```

RT genes 1-5.":
RL Bur. J. Biochem. 220:615-621(1994).
CC -1- SIMILARITY: Belongs to the avidin/streptavidin family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; Z21612; -; NOT ANNOTATED CDS; Genomic DNA.
CC EMBL; Z21536; -; NOT ANNOTATED CDS; mRNA.
CC PIR; S42203; S42203.
CC HSSP; P02701; 1NON.
CC SMR; P56733; 26-147.
CC Ensembl; ENSGALG0000002441; Gallus gallus.
CC InterPro; IPR005469; Avidin.
CC InterPro; IPR005468; Avidin/str.
CC Pfam; PF01382; Avidin; 1.
CC PRINTS; PR00709; Avidin.
CC PROSITE; PS00577; AVIDIN; 1.
CC Biocin; Glycoprotein, Multigene family; Signal.
CC SIGNAL; 1 24 Potential.
CC CHAIN; 25 150 Avidin-related protein 3.
CC BINDING; 57 57 Biotin (By similarity).
CC CARBOHYD; 93 93 N-linked (GlcNAc...) (Potential).
CC CARBOHYD; 141 141 N-linked (GlcNAc...) (Potential).
CC SEQUENCE; 150 AA; 16657 MW; 84DC03926A6BE21C CRC64;

Query Match 22.4%; Score 461; DB 1; Length 150;
Best Local Similarity 71.1%; Pred. No. 2.4e-20;
Matches 91; Conservative 10; Mismatches 25; Indels 2; Gaps 1;

QY 273 ARKSLGKWNNDGSMNTTGA VNSRGFTGTITAVATSNIEKESPLHGONTINRT 332
DB 25 ARKSLGKWNNDGSMNTTGA VNSRGFTGTITAVATSNIEKESPLHGONTINRT 332
QY 333 OPTGFTVNMKFSSTVFTGQCFLDRNGKEVLKTMMLRSSVNDIGDWKATRVGINIF 392
DB 83 OPTGFTVNMKFSSTVFTGQCFLDRNGKEVLKTMMLRSSVNDIGDWKATRVGINIF 142
QY 393 TRLRTQKE 400
DB 143 TRLRTQKE 150

RESULT 12
AVR7_CHICK STANDARD; PRT; 150 AA.
AC P56736; Q9M6V4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Avidin-related protein 7 precursor.
GN Name=AVR7;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CC NCBI_TaxID=9031;
CC [1]
CC NUCLEOTIDE SEQUENCE.
CC STRAIN=Rhode Island;
CC MEDLINE=21070478; PubMed=11167523;
CC Ahlroth M.K., Kola E.H., Ewald D., Meabanda J., Sazanov A., Fries R.,
CC Kuitto M.S.;
CC "Characterization and chromosomal localization of the chicken avidin
CC gene family.";
CC Nucleic Acids Res. 31:367-375(2003).
CC -1- SIMILARITY: Belongs to the avidin/streptavidin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC removed.
CC -----
CC EMBL; AJ237659; CAB39894.1; -; Genomic DNA.
CC HSSP; P02701; 1NON.
CC SMR; P56736; 26-147.
CC Ensembl; ENSGALG0000002441; Gallus gallus.
CC InterPro; IPR005469; Avidin.
CC InterPro; IPR005468; Avidin/str.
CC Pfam; PF01382; Avidin; 1.
CC PRINTS; PR00709; Avidin.
CC PROSITE; PS00577; AVIDIN; 1.
CC Biocin; Glycoprotein; Multigene family; Signal.
CC SIGNAL; 1 24 Potential.
CC CHAIN; 25 150 Avidin-related protein 7.
CC BINDING; 57 57 Biotin (By similarity).
CC CARBOHYD; 41 41 N-linked (GlcNAc...) (Potential).
CC CARBOHYD; 54 54 N-linked (GlcNAc...) (Potential).
CC CARBOHYD; 93 93 N-linked (GlcNAc...) (Potential).
CC CARBOHYD; 141 141 N-linked (GlcNAc...) (Potential).
CC SEQUENCE; 150 AA; 16543 MW; 30F335611F65923D CRC64;

Query Match 22.4%; Score 461; DB 1; Length 150;
Best Local Similarity 70.3%; Pred. No. 2.4e-20;
Matches 90; Conservative 10; Mismatches 26; Indels 2; Gaps 1;

QY 273 ARKSLGKWNNDGSMNTTGA VNSRGFTGTITAVATSNIEKESPLHGONTINRT 332
DB 25 ARKSLGKWNNDGSMNTTGA VNSRGFTGTITAVATSNIEKESPLHGONTINRT 332
QY 333 OPTGFTVNMKFSSTVFTGQCFLDRNGKEVLKTMMLRSSVNDIGDWKATRVGINIF 392
DB 83 OPTGFTVNMKFSSTVFTGQCFLDRNGKEVLKTMMLRSSVNDIGDWKATRVGINIF 142
QY 393 TRLRTQKE 400
DB 143 TRLRTQKE 150

RESULT 13
AVR1_CHICK STANDARD; PRT; 150 AA.
AC O13153;
DT 15-JUL-1999 (Rel. 38, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Avidin-related protein 1 precursor.
GN Name=AVR1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CC NCBI_TaxID=9031;
CC [1]
CC NUCLEOTIDE SEQUENCE.
CC TISSUE=Oviduct;
CC MEDLINE=88260103; PubMed=2838690; DOI=10.1016/0022-4731(88)90071-4;
CC Keinaenen R.A., Laukkanen M.-L., Kulomaa M.S.;
CC "Molecular cloning of three structurally related genes for chicken
CC avidin.";
CC J. Steroid Biochem. 30:17-21(1988).
CC [2]
CC NUCLEOTIDE SEQUENCE.
CC STRAIN=White leghorn; TISSUE=Oviduct;
CC MEDLINE=94170814; PubMed=8125122;
CC Keinaenen R.A., Wallen M.J., Kristo P.A., Laukkanen M.O.,
CC Toimela T.A., Helenius M.A., Kulomaa M.S.;
CC "Molecular cloning and nucleotide sequence of chicken avidin-related
CC genes 1-5.";
CC Bur. J. Biochem. 220:615-621(1994).
CC -1- SIMILARITY: Belongs to the avidin/streptavidin family.
CC -----

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CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL, 221611; -; NOT ANNOTATED CDS; Genomic_DNA.

DR EMBL, 297063; CAB09758.1; -; mRNA.

DR PIR, S42201; S42201.

DR HSPB, P02701; INON.

DR Ensembl, ENSGALG00000002441; Gallus gallus.

DR InterPro, IPR005469; Avidin.

DR InterPro, IPR005468; Avidin/str.

DR Pfam, PF01382; Avidin. 1.

DR PRINTS, PR00709; AVIDIN.

DR PROSITE, PS00577; AVIDIN. 1.

KW Biotin; Glycoprotein; Multigene family; Signal.

FT SIGNAL 1 24 Potential.

FT CHAIN 1 25 Avidin-related protein 1.

FT BINDING 57 57 Biotin (By similarity).

FT CARBOHYD 54 54 N-linked (GlcNAc...) (potential).

FT CARBOHYD 67 67 N-linked (GlcNAc...) (potential).

FT CARBOHYD 93 93 N-linked (GlcNAc...) (potential).

FT CARBOHYD 141 141 N-linked (GlcNAc...) (potential).

FT CARBOHYD 150 AA; 16468 MW; 7754838089581F6 CRC64;

SC SEQUENCE

Query Match 22.0%; Score 453; DB 1; Length 150;

Best Local Similarity 68.8%; Pred. No. 8.4e-20;

Matches 88; Conservative 10; Mismatches 28; Indels 2; Gaps 1;

273 ARKCSLTGKMTNDLGSNMITGAVNSRGFTGYITAVTATSNBIKESPLHGTONTINKRT 332

25 ARKCSLTGKMTNDLGSNMITGAVNSRGFTGYITAVTATSNBIKESPLHGTONTINKRT 82

333 OPTFGFTYHMFSESTSVFVGQCFYDRSGKEVLTMTLIRSVNDIGDDMKATRVGINF 392

83 OPTFGFTYHMFSESTSVFVGQCFYDRSGKEVLTMTLIRSVNDIGDDMKATRVGINF 142

393 TRLRTQKE 400

143 TRQRTVEE 150

Db

RESULT 14

AVR6 CHICK STANDARD; PRT; 150 AA.

ID AVR6 CHICK STANDARD; PRT; 150 AA.

AC P56735;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Avidin-related protein 6 precursor.

GN Name=AVR6;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OC NCBI_TaxID=9031;

OX [1]

NP NUCLEOTIDE SEQUENCE.

RP STRAIN=Rhode Island;

RC MEDLINE=21070478; PubMed=1167523;

RA Ahlroth M.K., Kola E.H., Ewald D., Masabanda J., Sazanov A., Fries R.,

RA Kulomaa M.S.;

RT "Characterization and chromosomal localization of the chicken avidin

RT gene family.";

RL Antim. Genet. 31:367-375(2000).

CC -1- SIMILARITY: Belongs to the avidin/streptavidin family.

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DR EMBL, AJ237658; CAB39893.1; -; Genomic_DNA.

DR HSPB, P02701; INON.

DR Ensembl, ENSGALG00000002441; Gallus gallus.

DR InterPro, IPR005469; Avidin.

DR InterPro, IPR005468; Avidin/str.

DR Pfam, PF01382; Avidin. 1.

DR PRINTS, PR00709; AVIDIN.

DR PROSITE, PS00577; AVIDIN. 1.

KW Biotin; Glycoprotein; Multigene family; Signal.

FT SIGNAL 1 24 Potential.

FT CHAIN 1 25 Avidin-related protein 6.

FT BINDING 57 57 Biotin (By similarity).

FT CARBOHYD 54 54 N-linked (GlcNAc...) (potential).

FT CARBOHYD 93 93 N-linked (GlcNAc...) (potential).

FT CARBOHYD 141 141 N-linked (GlcNAc...) (potential).

FT CARBOHYD 150 AA; 16528 MW; C0F3357D6291B150 CRC64;

SC SEQUENCE

Query Match 21.9%; Score 451; DB 1; Length 150;

Best Local Similarity 68.8%; Pred. No. 9.6e-20;

Matches 88; Conservative 11; Mismatches 27; Indels 2; Gaps 1;

273 ARKCSLTGKMTNDLGSNMITGAVNSRGFTGYITAVTATSNBIKESPLHGTONTINKRT 332

25 ARKCSLTGKMTNDLGSNMITGAVNSRGFTGYITAVTATSNBIKESPLHGTONTINKRT 82

333 OPTFGFTYHMFSESTSVFVGQCFYDRSGKEVLTMTLIRSVNDIGDDMKATRVGINF 392

83 OPTFGFTYHMFSESTSVFVGQCFYDRSGKEVLTMTLIRSVNDIGDDMKATRVGINF 142

393 TRLRTQKE 400

143 TRQRTVEE 150

Db

RESULT 15

AVR2 CHICK STANDARD; PRT; 150 AA.

ID AVR2 CHICK STANDARD; PRT; 150 AA.

AC P56732; 0546L5;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Avidin-related protein 2 precursor.

GN Name=AVR2;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OC NCBI_TaxID=9031;

OX [1]

NP NUCLEOTIDE SEQUENCE.

RP STRAIN=White leghorn; TISSUE=Oviduct;

RC MEDLINE=94170814; PubMed=8125122;

RA Keinaenen R.A., Wallen M.J., Kristo P.A., Laukkanen M.O.,

RA Toimela T.A., Helenus M.A., Kulomaa M.S.;

RT "Molecular cloning and nucleotide sequence of chicken avidin-related

RT genes 1-5.";

RL Eur. J. Biochem. 220:615-621(1994).

CC -1- SIMILARITY: Belongs to the avidin/streptavidin family.

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CC removed.

DR EMBL; Z21554; -; NOT ANNOTATED CDS; Genomic_DNA.
 DR EMBL; Z21535; -; NOT ANNOTATED CDS; mRNA.
 DR EMBL; AJ311648; CAC34570.1; -; Genomic_DNA.
 DR PIR; S42202; S42202.
 DR HSSP; P02701; INON.
 DR Ensembl; ENSGALG0000002441; Gallus gallus.
 DR InterPro; IPR005469; Avidin.
 DR InterPro; IPR005468; Avidin/str.
 DR Pfam; PF01382; Avidin; 1.
 DR PRINTS; PR00709; AVIDIN.
 DR PROSITE; PS00577; AVIDIN; 1.
 KM Biotin; Glycoprotein; Multigene family; Signal.
 FT SIGNAL 1 24 Potential.
 FT CHAIN 25 150 Avidin-related protein 2.
 FT BINDING 57 57 Biotin (By similarity).
 FT CARBOHYD 67 67 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 150 AA; 16435 MW; 763D1E2B1A93A66D CRC64;

Query Match 21.2%; Score 436; DB 1; Length 150;
 Best Local Similarity 67.2%; Pred. No. 7.8e-19;
 Matches 86; Conservative 11; Mismatches 29; Indels 2; Gaps 1;

QY 273 ARKCSLTGKWTNDIGSNMTIGAVNSRGEFTGYTATATSNIEKESPLHGTONTINKT 332
 Db 25 ARKCSLTGEMNDLGSIMTIGAVNDNGEFDGYITAVADNPGNITLSPLLGIQH--KRAS 82
 QY 333 OPTGFTNNMKFSESTYVFTQCCTIDRNGKEVLKTMWLLRSSVNDIGDDMKATRVGINIF 392
 Db 83 OPTGFTVHMFSESTSVFVGQCFVDRSGKEVLKTKWLQRLAVDDISDDMTATRVGNNDP 142
 QY 393 TRLRTQKE 400
 Db 143 TROHTVEE 150

Search completed: February 16, 2006, 17:05:01
 Job time : 234 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 17:05:18 ; Search time 47 Seconds
(without alignments)
703.623 Million cell updates/sec

Title: US-10-618-570-2

Perfect score: 2059

Sequence: 1 MAQMDPFDQEDTSDCTES.....DKATRVGINIFRLRTQKE 400

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*\n2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*\n3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*\n4: /cgn2_6/ptodata/1/1aa/RTUS_COMB.pep:*\n5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*\n6: /cgn2_6/ptodata/1/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1381	67.1	349	6	5510466-2 Patent No. 5510466
2	1381	67.1	453	6	5510466-4 Patent No. 5510466
3	1047.5	50.9	451	1	US-08-154-365-2 Sequence 2, Appl1
4	1047.5	50.6	358	1	US-08-453-117-4 Sequence 4, Appl1
5	1047.5	50.6	358	1	US-08-948-222-4 Sequence 4, Appl1
6	1047.5	50.6	358	1	US-08-973-145-4 Sequence 4, Appl1
7	1047.5	50.6	358	4	PCT-US96-08081-4 Sequence 4, Appl1
8	1047.5	50.6	358	2	US-09-949-016-9258 Sequence 9258, Ap
9	1047.5	50.6	451	1	US-08-453-117-2 Sequence 2, Appl1
10	1047.5	50.6	451	1	US-08-948-222-2 Sequence 2, Appl1
11	1047.5	50.6	451	1	US-08-973-145-2 Sequence 2, Appl1
12	1047.5	50.6	451	2	US-09-276-400-10 Sequence 10, Appl
13	1047.5	50.6	451	2	US-09-448-076-10 Sequence 10, Appl
14	1047.5	50.6	451	2	US-09-702-572-10 Sequence 10, Appl
15	1047.5	50.6	451	4	PCT-US96-08081-2 Sequence 2, Appl1
16	678	32.9	152	2	US-08-831-399-4 Sequence 4, Appl1
17	678	32.9	152	2	US-09-366-862-4 Sequence 4, Appl1
18	678	32.9	152	2	US-09-368-772-4 Sequence 4, Appl1
19	138.5	6.7	159	2	US-08-628-540-1 Sequence 1, Appl1
20	138.5	6.7	159	2	US-08-948-097-17 Sequence 17, Appl
21	138.5	6.7	159	2	US-08-941-100-1 Sequence 1, Appl1
22	138.5	6.7	159	2	US-08-941-100-5 Sequence 5, Appl1
23	138.5	6.7	159	2	US-09-381-430-2 Sequence 2, Appl1
24	138.5	6.7	183	2	US-08-831-399-2 Sequence 2, Appl1
25	138.5	6.7	183	2	US-09-366-862-2 Sequence 2, Appl1
26	138.5	6.7	183	2	US-09-368-772-2 Sequence 2, Appl1
27	138.5	6.7	183	4	PCT-US93-05240-14 Sequence 14, Appl

28	138.5	6.7	183	6	5168049-5 Patent No. 5168049
29	138.5	6.7	415	1	US-08-491-988-7 Sequence 7, Appl1
30	138.5	6.7	421	2	US-09-938-270B-1 Sequence 1, Appl1
31	138.5	6.7	435	1	US-08-491-988-5 Sequence 5, Appl1
32	138.5	6.6	128	1	US-08-211-833-2 Sequence 2, Appl1
33	135.5	6.6	128	1	US-08-434-718-2 Sequence 2, Appl1
34	135.5	6.6	128	2	US-08-831-399-16 Sequence 16, Appl
35	135.5	6.6	128	2	US-09-366-862-16 Sequence 16, Appl
36	135.5	6.6	128	2	US-09-368-772-16 Sequence 16, Appl
37	135.5	6.6	402	1	US-08-491-988-9 Sequence 9, Appl1
38	135.5	6.6	10182	2	US-09-134-001C-3159 Sequence 3159, Ap
39	133	6.5	186	2	US-09-382-276-2 Sequence 2, Appl1
40	132.5	6.4	118	2	US-07-780-717C-7 Sequence 7, Appl1
41	131	6.4	186	2	US-09-382-276-3 Sequence 3, Appl1
42	130.5	6.3	183	2	US-09-382-276-1 Sequence 1, Appl1
43	130.5	6.3	183	2	US-09-285-867-1 Sequence 1, Appl1
44	129.5	6.3	1307	2	US-09-949-016-7561 Sequence 7561, Ap
45	123	6.0	2663	2	US-09-538-092-1252 Sequence 1252, Ap

ALIGNMENTS

```
RESULT 1
Patent No. 5510466
APPLICANT: KREIGER, MONTY;KODAMA, TATSUHIKO
TITLE OF INVENTION: SCAVENGER RECEPTOR PROTEIN AND ANTIBODY
THERETO
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,400
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 997,113
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 391,486
FILING DATE: 09-AUG-1989
APPLICATION NUMBER: 272,002
FILING DATE: 15-NOV-1988
SEQ ID NO:2
LENGTH: 349
5510466-2
67.1%; Score 1381; DB 6; Length 349;
Best Local Similarity 100.0%; Pred. No. 4.36-112; Indels 0; Gaps 0;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MAQMDPFDQEDTSDCTESYKFDARSVTALLPFPKNGPTLQERMSKYKTLITLYLIV 60
QY 61 FVLIPIIIGIYAQAOLKMETKNCCTGVSNADISPSPEKKGSGEDEMRPREAVERMSNM 120
DB 61 FVLIPIIIGIYAQAOLKMETKNCCTGVSNADISPSPEKKGSGEDEMRPREAVERMSNM 120
QY 61 FVLIPIIIGIYAQAOLKMETKNCCTGVSNADISPSPEKKGSGEDEMRPREAVERMSNM 120
DB 61 FVLIPIIIGIYAQAOLKMETKNCCTGVSNADISPSPEKKGSGEDEMRPREAVERMSNM 120
QY 121 ESRIOYLSDNENANLIDAKNFQSFSTTQRRNDVLFQNSLSSIOEHENITIGDISKLV 180
DB 121 ESRIOYLSDNENANLIDAKNFQSFSTTQRRNDVLFQNSLSSIOEHENITIGDISKLV 180
QY 121 ESRIOYLSDNENANLIDAKNFQSFSTTQRRNDVLFQNSLSSIOEHENITIGDISKLV 180
DB 121 ESRIOYLSDNENANLIDAKNFQSFSTTQRRNDVLFQNSLSSIOEHENITIGDISKLV 180
QY 181 GIANTVLDQSIETFLNGRVOENAFKQOEERKLEERLYNNAETIKSIDKQVYLEQIRK 240
DB 181 GIANTVLDQSIETFLNGRVOENAFKQOEERKLEERLYNNAETIKSIDKQVYLEQIRK 240
QY 241 GEMKLNITNDRLRKDEHSQTLKNITLLQG 272
DB 241 GEMKLNITNDRLRKDEHSQTLKNITLLQG 272
RESULT 2
Patent No. 5510466
APPLICANT: KREIGER, MONTY;KODAMA, TATSUHIKO
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; TITLE OF INVENTION: SCAVENGER RECEPTOR PROTEIN AND ANTIBODY
; THESETO
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,400
; FILING DATE: 16-SEP-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 997,113
; FILING DATE: 24-DEC-1992
; APPLICATION NUMBER: 391,486
; FILING DATE: 09-AUG-1989
; APPLICATION NUMBER: 272,002
; FILING DATE: 15-NOV-1988
; SEQ ID NO: 4:
; LENGTH: 453
; 5510466-4

Query Match          67.1%; Score 1381; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 6,38-112;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQMDPPDQEDTDSCTESYKFDARSVTALLPFPKNGPTLQERMSYKATLITLIV 60
DB 1 MAQMDPPDQEDTDSCTESYKFDARSVTALLPFPKNGPTLQERMSYKATLITLIV 60
QY 61 FVVLVPIIGIYAAOLLKMETKNCCTVGSVNAISPSPGKNGSEDEMRPREAVMERMSN 120
DB 61 FVVLVPIIGIYAAOLLKMETKNCCTVGSVNAISPSPGKNGSEDEMRPREAVMERMSN 120
QY 121 ESRIOYLSDEANMLDANKFONFSITTDQRFNDVLPQLNSLLSIOEHENIIGDISKSLV 180
DB 121 ESRIOYLSDEANMLDANKFONFSITTDQRFNDVLPQLNSLLSIOEHENIIGDISKSLV 180
QY 181 GIANTVLDLOFSIETLNGRVQENAFKQOEEMRKLEERTYNASAEIKSLDEQVYLEQEI 240
DB 181 GIANTVLDLOFSIETLNGRVQENAFKQOEEMRKLEERTYNASAEIKSLDEQVYLEQEI 240
QY 241 GEMKLNITNDRLKDMESHQTLKNITLLQG 272
DB 241 GEMKLNITNDRLKDMESHQTLKNITLLQG 272

RESULT 3
US-08-154-365-2
; Sequence 2, Application US/08154365
; Patent No. 5624904
; GENERAL INFORMATION:
; APPLICANT: Dunne, Dana W.
; APPLICANT: Resnick, David
; APPLICANT: Kreiger, Monty
; APPLICANT: Joiner, Keith A.
; TITLE OF INVENTION: Method for Treating Gram-Positive
; TITLE OF INVENTION: Septicemia
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Ga
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/154,365
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
```

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; REFERENCE/DOCKET NUMBER: MIT6392
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; PUBLICATION INFORMATION:
; AUTHORS: Ashkenae, et al.
; JOURNAL: J. Lipid Res.
; VOLUME: 34
; PAGES: 983-1000
; DATE: 1993
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 451
; US-08-154-365-2

Query Match          50.9%; Score 1047.5; DB 1; Length 451;
Best Local Similarity 72.5%; Pred. No. 7,48-83;
Matches 198; Conservative 40; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQMDPPDQEDTDSCTESYKFDARSVTALLPFPKNGPTLQERMSYKATLITLIV 60
DB 1 MEQMDHFHQEDTDSCTESYKFDARSVTALLPFPKNGPTLQERMSYKATLITLIV 60
QY 61 FVVLVPIIGIYAAOLLKMETKNCCTVGSVNA-DISPSPGKNGSEDEMRPREAVMERMSN 119
DB 61 FVVLVPIIGIYAAOLLKMETKNCCTVGSVNA-DISPSPGKNGSEDEMRPREAVMERMSN 119
QY 120 MESRIQYLSDEANMLDANKFONFSITTDQRFNDVLPQLNSLLSIOEHENIIGDISKSL 179
DB 120 MESRIQYLSDEANMLDANKFONFSITTDQRFNDVLPQLNSLLSIOEHENIIGDISKSL 179
QY 181 ISLNTTLLDLOLNTENNGKIOENTPFQOEISKLEBRYVNSAIVAMKGVYLEQEI 240
DB 181 ISLNTTLLDLOLNTENNGKIOENTPFQOEISKLEBRYVNSAIVAMKGVYLEQEI 240
QY 240 GEMKLNITNDRLKDMESHQTLKNITLLQG 272
DB 241 GEMKLNITNDRLKDMESHQTLKNITLLQG 272

RESULT 4
US-08-453-117-4
; Sequence 4, Application US/08453117
; Patent No. 5683903
; GENERAL INFORMATION:
; APPLICANT: Lysko, Paul G.
; APPLICANT: Elshourbagy, Nabli A.
; APPLICANT: Branner, Mary E.
; TITLE OF INVENTION: Attachment Enhanced 293 Cells
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham - Corporate Patents
; STREET: Mailcode - UM2220, 709 Swedeland Road
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19406-5090
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
```

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,117
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jervls, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: SBC-P50338
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-453-117-4

Query Match      50.6%; Score 1042.5; DB 1; Length 358;
Best Local Similarity 72.2%; Pred. No. 1.4e-82;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDFPDQEDTSCSVEKFDARSVTALLPPHPKNGPTIOEEMKSYKTLITLYLV 60
DB 1 MEQWDFHNOQEDTSCSVEKFDARSMTALLPPHPKNSPSIQEKLKSKFALLIYLYLV 60
QY 61 FVVLVPIIGIVAQAOLKMKETKCTGVSA-VNA-DISPSPEKGSGSEDEMRFREAVERNRN 119
DB 61 FAVLPLIGIVAQAOLKMKETKCSVSTNANDITQSLTGKNDSEEMRFQEVFMEHNSN 120
QY 120 MESRIQYLSNDNANLIDAKNFQSFITTDQRPNDVLPQNLSSLSIOEHENIIGDISKL 179
DB 121 MEKRIQHLIDMANLMDTEHFQNFMTTDDQRPNDILQLSTLFSSVQGHNAIDISKL 180
QY 180 VGLNTTVLDLQSIETLNGRVOENAFKQOEEMKLEERYNYSAEIKSLDEKQVLEQEI 239
DB 181 ISLNTTLLDLQNTINLNGKIQENTFKQOEISKLEERYNYSAEIMAKEQVHLEQEI 240
QY 240 KGEMLNNITNDLRKDWESQTLKNITLLQG 272
DB 241 KGEVYLNNTITDRLKDWESQTLKNITLLIQG 273

RESULT 5
US-08-948-222-4
Sequence 4, Application US/08948222
Patent No. 5863798
GENERAL INFORMATION:
APPLICANT: Lyeko, Paul G.
APPLICANT: Eishourdegy, Nabil A.
APPLICANT: Brauer, Mary B.
TITLE OF INVENTION: Attachment Enhanced 293 Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Smithkline Beecham - Corporate Patents
ADDRESSES: U.S.
STREET: Mailcode - UW2220, 709 Swedeland Road
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19406-5090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,222
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/453,117
```

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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jervls, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: SBC-P50338
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-948-222-4

Query Match      50.6%; Score 1042.5; DB 1; Length 358;
Best Local Similarity 72.2%; Pred. No. 1.4e-82;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDFPDQEDTSCSVEKFDARSVTALLPPHPKNGPTIOEEMKSYKTLITLYLV 60
DB 1 MEQWDFHNOQEDTSCSVEKFDARSMTALLPPHPKNSPSIQEKLKSKFALLIYLYLV 60
QY 61 FVVLVPIIGIVAQAOLKMKETKCTGVSA-VNA-DISPSPEKGSGSEDEMRFREAVERNRN 119
DB 61 FAVLPLIGIVAQAOLKMKETKCSVSTNANDITQSLTGKNDSEEMRFQEVFMEHNSN 120
QY 120 MESRIQYLSNDNANLIDAKNFQSFITTDQRPNDVLPQNLSSLSIOEHENIIGDISKL 179
DB 121 MEKRIQHLIDMANLMDTEHFQNFMTTDDQRPNDILQLSTLFSSVQGHNAIDISKL 180
QY 180 VGLNTTVLDLQSIETLNGRVOENAFKQOEEMKLEERYNYSAEIKSLDEKQVLEQEI 239
DB 181 ISLNTTLLDLQNTINLNGKIQENTFKQOEISKLEERYNYSAEIMAKEQVHLEQEI 240
QY 240 KGEMLNNITNDLRKDWESQTLKNITLLQG 272
DB 241 KGEVYLNNTITDRLKDWESQTLKNITLLIQG 273

RESULT 6
US-08-973-145-4
Sequence 4, Application US/08973145
Patent No. 5919636
GENERAL INFORMATION:
APPLICANT: Lyeko, Paul G.
APPLICANT: Eishourdegy, Nabil A.
APPLICANT: Brauer, Mary B.
TITLE OF INVENTION: Attachment Enhanced 293 Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Smithkline Beecham - Corporate Patents U.S.
STREET: Mailcode - UW2220, 709 Swedeland Road
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19406-5090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,145
FILING DATE: 26-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth J. Hecht
REGISTRATION NUMBER: P-41, 824
REFERENCE/DOCKET NUMBER: P50338
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5009
```

TELEFAX: (610) 270-5090
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 358 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-973-145-4

Query Match 50.6%; Score 1042.5; DB 1; Length 358;
 Best Local Similarity 72.2%; Pred. No. 1.4e-82;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQMDPDPQOEDPDSCTESVYKFDARSVTALLPFPKPKGPTLOEMKSYKTAALTLYLYIV 60
 DB 1 MEQMDHFNQOEDPDSCTESVYKFDARSMTALLPFPKPSPSLOEKLKSPKKAALTLYLYIV 60
 QY 61 FVLVPIIGIYVAOQLKMETKCTVGSVNA-DISPEPGKNGSEDEMRPREAVEMRSN 119
 DB 61 FVLVPIIGIYVAOQLKMETKCTVGSVNA-DISPEPGKNGSEDEMRPREAVEMRSN 120
 QY 120 MESRIQYISDNEANILDAKNFONFSITTDQRFNDVLPQNLSSIOEHENIGDISKSL 179
 DB 121 MEKRIQHLDEANILMDTEHFONFSMTTDQRFNDILQLSTLFSVQGHNAIDISKSL 180
 QY 180 VGLNTTVLDLQFSIETLNGRVOENAFKQOEMRKLEIRIYNASAEIKSLDEKQVYLEOEI 239
 DB 181 ISLNTTLLDLQNLINENLNGKIQENTFKQOEBISKLEERVYVNSAIIAMKEQVHLEOEI 240
 QY 240 KGEKMLNNITNDRLKDMESQTLKNITLLQG 272
 DB 241 KGEVAVLNNTNDRLKDMESQTLKNITLLQG 273

RESULT 7

PCT-US96-08081-4
 Sequence 4, Application PC/TUS9608081
 GENERAL INFORMATION:
 APPLICANT: SmithKline Beecham Corporation
 TITLE OF INVENTION: Attachment Enhanced 293 Cells
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham - Corporate Patents U.S.
 STREET: Mailcode - UM2220, 709 Swedeland Road
 CITY: King of Prussia
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19406-5090
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/08081
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Jervis, Herbert H.
 REGISTRATION NUMBER: 31,171
 REFERENCE/DOCKET NUMBER: P50338
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 270-5019
 TELEFAX: (610) 270-5090
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 358 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-08081-4

Query Match 50.6%; Score 1042.5; DB 4; Length 358;

Best Local Similarity 72.2%; Pred. No. 1.4e-82;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQMDPDPQOEDPDSCTESVYKFDARSVTALLPFPKPKGPTLOEMKSYKTAALTLYLYIV 60
 DB 1 MEQMDHFNQOEDPDSCTESVYKFDARSMTALLPFPKPSPSLOEKLKSPKKAALTLYLYIV 60
 QY 61 FVLVPIIGIYVAOQLKMETKCTVGSVNA-DISPEPGKNGSEDEMRPREAVEMRSN 119
 DB 61 FVLVPIIGIYVAOQLKMETKCTVGSVNA-DISPEPGKNGSEDEMRPREAVEMRSN 120
 QY 120 MESRIQYISDNEANILDAKNFONFSITTDQRFNDVLPQNLSSIOEHENIGDISKSL 179
 DB 121 MEKRIQHLDEANILMDTEHFONFSMTTDQRFNDILQLSTLFSVQGHNAIDISKSL 180
 QY 180 VGLNTTVLDLQFSIETLNGRVOENAFKQOEMRKLEIRIYNASAEIKSLDEKQVYLEOEI 239
 DB 181 ISLNTTLLDLQNLINENLNGKIQENTFKQOEBISKLEERVYVNSAIIAMKEQVHLEOEI 240
 QY 240 KGEKMLNNITNDRLKDMESQTLKNITLLQG 272
 DB 241 KGEVAVLNNTNDRLKDMESQTLKNITLLQG 273

RESULT 8

US-09-949-016-9258
 Sequence 9258, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYNORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CLO01307
 CURRENT APPLICATION NUMBER: US/09/949,016
 PRIOR FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 9258
 LENGTH: 362
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-9258

Query Match 50.6%; Score 1042.5; DB 2; Length 362;
 Best Local Similarity 72.2%; Pred. No. 1.5e-82;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQMDPDPQOEDPDSCTESVYKFDARSVTALLPFPKPKGPTLOEMKSYKTAALTLYLYIV 60
 DB 5 MEQMDHFNQOEDPDSCTESVYKFDARSMTALLPFPKPSPSLOEKLKSPKKAALTLYLYIV 64
 QY 61 FVLVPIIGIYVAOQLKMETKCTVGSVNA-DISPEPGKNGSEDEMRPREAVEMRSN 119
 DB 65 FVLVPIIGIYVAOQLKMETKCTVGSVNA-DISPEPGKNGSEDEMRPREAVEMRSN 124
 QY 120 MESRIQYISDNEANILDAKNFONFSITTDQRFNDVLPQNLSSIOEHENIGDISKSL 179
 DB 125 MEKRIQHLDEANILMDTEHFONFSMTTDQRFNDILQLSTLFSVQGHNAIDISKSL 184
 QY 180 VGLNTTVLDLQFSIETLNGRVOENAFKQOEMRKLEIRIYNASAEIKSLDEKQVYLEOEI 239
 DB 185 ISLNTTLLDLQNLINENLNGKIQENTFKQOEBISKLEERVYVNSAIIAMKEQVHLEOEI 244
 QY 240 KGEKMLNNITNDRLKDMESQTLKNITLLQG 272
 DB 245 KGEVAVLNNTNDRLKDMESQTLKNITLLQG 277

RESULT 9

US-08-453-117-2

Sequence 2, Application US/08453117

Patent No. 5683903

GENERAL INFORMATION:

APPLICANT: Lysko, Paul G.

APPLICANT: Elshourbagy, Nabil A.

APPLICANT: Brauner, Mary E.

TITLE OF INVENTION: Attachment Enhanced 293 Cells

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham - Corporate Patents

ADDRESS: U.S.

STREET: Mailcode - UM2220, 709 Swedeland Road

CITY: King of Prussia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19406-5090

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/453,117

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jarvis, Herbert H.

REGISTRATION NUMBER: 31,171

REFERENCE/DOCKET NUMBER: SBC-P50338

TELEPHONE: (610) 270-5019

TELEFAX: (610) 270-5090

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 451 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-453-117-2

Query Match 50.6%; Score 1042.5; DB 1; Length 451;

Best Local Similarity 72.2%; Pred. No. 2e-82; Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Db 1 MAOWDPDPOQEDTDSCTESVFKDARSVTALLPPHPKNGPTLOERKSKYKALTITLYLV 60

Db 1 MEQWDFHNOQEDTDSCTESVFKDARSVTALLPPHPKNGPTLOERKSKYKALTITLYLV 60

Db 61 FVLVPIIGIIVAQAOLKMKETKCTGVSVA-DISPSPEGKNGSDEMRPREAVERMSN 119

Db 61 FVLVPIIGIIVAQAOLKMKETKCTGVSVA-DISPSPEGKNGSDEMRPREAVERMSN 119

Db 120 MESRIQVSDNEANLIDAKNFONESTTDORENDVLFQINSLSIOEHENIIGDISKL 179

Db 121 MEKRIQVSDNEANLIDAKNFONESTTDORENDVLFQINSLSIOEHENIIGDISKL 180

Db 180 VGLNTTVLDLOFISITLNGRVOENAFKQOEEMKLEERYNVAABIKSIDEROVYLEOEI 239

Db 181 ISLNTTVLDLOFISITLNGRVOENAFKQOEEMKLEERYNVAABIKSIDEROVYLEOEI 240

Db 240 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

APPLICANT: Lysko, Paul G.

APPLICANT: Elshourbagy, Nabil A.

APPLICANT: Brauner, Mary E.

TITLE OF INVENTION: Attachment Enhanced 293 Cells

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham - Corporate Patents

ADDRESS: U.S.

STREET: Mailcode - UM2220, 709 Swedeland Road

CITY: King of Prussia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19406-5090

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/948,222

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/453,117

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jarvis, Herbert H.

REGISTRATION NUMBER: 31,171

REFERENCE/DOCKET NUMBER: SBC-P50338

TELEPHONE: (610) 270-5019

TELEFAX: (610) 270-5090

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 451 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-948-222-2

Query Match 50.6%; Score 1042.5; DB 1; Length 451;

Best Local Similarity 72.2%; Pred. No. 2e-82; Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Db 1 MAOWDPDPOQEDTDSCTESVFKDARSVTALLPPHPKNGPTLOERKSKYKALTITLYLV 60

Db 1 MEQWDFHNOQEDTDSCTESVFKDARSVTALLPPHPKNGPTLOERKSKYKALTITLYLV 60

Db 61 FVLVPIIGIIVAQAOLKMKETKCTGVSVA-DISPSPEGKNGSDEMRPREAVERMSN 119

Db 61 FVLVPIIGIIVAQAOLKMKETKCTGVSVA-DISPSPEGKNGSDEMRPREAVERMSN 119

Db 120 MESRIQVSDNEANLIDAKNFONESTTDORENDVLFQINSLSIOEHENIIGDISKL 179

Db 121 MEKRIQVSDNEANLIDAKNFONESTTDORENDVLFQINSLSIOEHENIIGDISKL 180

Db 180 VGLNTTVLDLOFISITLNGRVOENAFKQOEEMKLEERYNVAABIKSIDEROVYLEOEI 239

Db 181 ISLNTTVLDLOFISITLNGRVOENAFKQOEEMKLEERYNVAABIKSIDEROVYLEOEI 240

Db 240 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 272

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

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Db 241 KGEVKVANNITNDLRKDKWEHSQTLRNITLIG 273

RESULT 10

US-08-948-222-2

Sequence 2, Application US/08948222

Patent No. 5863798

GENERAL INFORMATION:

APPLICANT: Lysko, Paul G.

APPLICANT: Elshourbagy, Nabil A.

APPLICANT: Brauner, Mary E.

TITLE OF INVENTION: Attachment Enhanced 293 Cells

NUMBER OF SEQUENCES: 4

RESULT 11

US-08-973-145-2

Sequence 2, Application US/08973145

Patent No. 5919636

GENERAL INFORMATION:

APPLICANT: Lysko, Paul G.

APPLICANT: Elshourbagy, Nabil A.

APPLICANT: Brauner, Mary E.

TITLE OF INVENTION: Attachment Enhanced 293 Cells
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham - Corporate Patents U.S.
 STREET: Mailcode - UW2220, 709 Swedeland Road
 CITY: King of Prussia
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19406-5090
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/973,145
 FILING DATE: 26-NOV-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth J. Hecht
 REGISTRATION NUMBER: P-41, 824
 REFERENCE/DOCKET NUMBER: P50338
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 270-5009
 TELEFAX: (610) 270-5090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 451 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-973-145-2

Query Match 50.6%; Score 1042.5; DB 1; Length 451;
 Best Local Similarity 72.2%; Pred. No. 2e-82; Indels 1; Gaps 1;
 Matches 197; Conservative 41; Mismatches 34;

QY 1 MAQWDFPDQEDTDSCTESVYKFDARSVTALLPPHPKNGPTLQERMSYKATLITLYLIV 60
 DB 1 MEQWDFHNOQEDTDSCTESVYKFDARSMTALLPPHPKNSPSIQETLKSFKALLIALYLLV 60
 QY 61 FVVLVPIIGIYAAQLKMETKNCCTVGSYNA-DISSPBGKNGSGDEMRFRPAVVERNSN 119
 DB 61 FAVLIPILIGIYAAQLKMETKNCSSVSTNADITQSLTGKNDSEEMRFQEVFMEHNSN 120
 QY 120 MESRIQVSDNEANLIDAKNFQNSITTDQRFNDVLPOLNSLSIOEHENIIGDISKSL 179
 DB 121 MEKRIQHLIDNEANLMDTEHFQNSMTTDQRFNDILQLSTLFSVOGHNAIDISKSL 180
 QY 180 VGLNTTVLDLQFSIETTLNGRVOENAFKQOEMRKLEERIYNASAEIKSLDEKQVYLEQEI 239
 DB 181 ISLNTTLLDLQNLINENLNGKIQENTFKQOEISKLEERYVNSAEIMAMKEQVHLEQEI 240
 QY 240 KGEKMLNNITNDRLKQWESQTLKNITLLQG 272
 DB 241 KGEVAVLNNITNDRLKQWESQTLKNITLLQG 273

RESULT 12
 US-09-276-400-10
 Sequence 10, Application US/09276400
 Patent No. 6140056
 GENERAL INFORMATION:
 APPLICANT: Rhododoust, Mehran
 TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND
 TITLE OF INVENTION: US9276400
 FILE REFERENCE: WNI-073
 CURRENT APPLICATION NUMBER: US/09/276,400
 CURRENT FILING DATE: 1999-03-25
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 10
 LENGTH: 451

TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-276-400-10

Query Match 50.6%; Score 1042.5; DB 2; Length 451;
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 Matches 197; Conservative 41; Mismatches 34;

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 DB 1 MEQWDFHNOQEDTDSCTESVYKFDARSMTALLPPHPKNSPSIQETLKSFKALLIALYLLV 60
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 DB 61 FAVLIPILIGIYAAQLKMETKNCSSVSTNADITQSLTGKNDSEEMRFQEVFMEHNSN 120
 QY 120 MESRIQVSDNEANLIDAKNFQNSITTDQRFNDVLPOLNSLSIOEHENIIGDISKSL 179
 DB 121 MEKRIQHLIDNEANLMDTEHFQNSMTTDQRFNDILQLSTLFSVOGHNAIDISKSL 180
 QY 180 VGLNTTVLDLQFSIETTLNGRVOENAFKQOEMRKLEERIYNASAEIKSLDEKQVYLEQEI 239
 DB 181 ISLNTTLLDLQNLINENLNGKIQENTFKQOEISKLEERYVNSAEIMAMKEQVHLEQEI 240
 QY 240 KGEKMLNNITNDRLKQWESQTLKNITLLQG 272
 DB 241 KGEVAVLNNITNDRLKQWESQTLKNITLLQG 273

RESULT 13
 US-09-448-076-10
 Sequence 10, Application US/09448076
 Patent No. 6300092
 GENERAL INFORMATION:
 APPLICANT: Rhododoust, Mehran et al.
 TITLE OF INVENTION: METHODS OF USE OF A NOVEL LYSYL OXIDASE-RELATED PROTEIN
 FILE REFERENCE: WNI-073CP
 CURRENT APPLICATION NUMBER: US/09/448,076
 CURRENT FILING DATE: 1999-11-23
 EARLIER APPLICATION NUMBER: 60/117,580
 EARLIER FILING DATE: 1999-01-27
 EARLIER APPLICATION NUMBER: 09/276,400
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 10
 LENGTH: 451
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-448-076-10

Query Match 50.6%; Score 1042.5; DB 2; Length 451;
 Best Local Similarity 72.2%; Pred. No. 2e-82; Indels 1; Gaps 1;
 Matches 197; Conservative 41; Mismatches 34;

QY 1 MAQWDFPDQEDTDSCTESVYKFDARSVTALLPPHPKNGPTLQERMSYKATLITLYLIV 60
 DB 1 MEQWDFHNOQEDTDSCTESVYKFDARSMTALLPPHPKNSPSIQETLKSFKALLIALYLLV 60
 QY 61 FVVLVPIIGIYAAQLKMETKNCCTVGSYNA-DISSPBGKNGSGDEMRFRPAVVERNSN 119
 DB 61 FAVLIPILIGIYAAQLKMETKNCSSVSTNADITQSLTGKNDSEEMRFQEVFMEHNSN 120
 QY 120 MESRIQVSDNEANLIDAKNFQNSITTDQRFNDVLPOLNSLSIOEHENIIGDISKSL 179
 DB 121 MEKRIQHLIDNEANLMDTEHFQNSMTTDQRFNDILQLSTLFSVOGHNAIDISKSL 180
 QY 180 VGLNTTVLDLQFSIETTLNGRVOENAFKQOEMRKLEERIYNASAEIKSLDEKQVYLEQEI 239
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 QY 240 KGEKMLNNITNDRLKQWESQTLKNITLLQG 272

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 17:06:02 / Search time 166 Seconds
(without alignments)
1006.818 Million cell updates/sec

Title: US-10-618-570-2

Perfect score: 2059
Sequence: 1 MAQWDPDFPDQEDTDCSTES.....DKATRVGINFTRLRQKE 400

Scoring table:

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Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA Main:

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- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBSCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2059	100.0	400	4	US-10-618-570-2
2	1042.5	50.6	358	5	US-10-326-186-6
3	1042.5	50.6	358	5	US-10-741-600-1394
4	1042.5	50.6	358	5	US-10-741-600-1397
5	1042.5	50.6	358	5	US-10-741-600-1398
6	1042.5	50.6	358	5	US-10-741-600-1396
7	1042.5	50.6	451	3	US-09-782-980-19
8	1042.5	50.6	451	3	US-09-909-743-10
9	1042.5	50.6	451	4	US-10-426-262-2
10	1042.5	50.6	451	4	US-10-423-543-80
11	1042.5	50.6	451	4	US-10-806-018-19
12	1042.5	50.6	451	5	US-10-741-600-1395
13	801	38.9	454	5	US-10-496-905-481
14	801	38.9	458	3	US-09-782-980-126
15	801	38.9	458	4	US-10-806-018-126
16	678	32.9	152	4	US-10-724-527-4
17	678	32.9	151	6	US-11-093-776-7
18	675	32.8	152	3	US-09-957-667-2
19	670	32.5	173	5	US-10-893-576-59
20	670	32.5	485	4	US-10-656-769-59
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22	204	9.9	495	4	US-10-468-335-2
23	204	9.9	517	4	US-10-138-588-66
24	201	9.8	495	5	US-10-496-905-444
25	169	8.2	244	4	US-10-326-186-8
26	168.5	8.2	234	4	US-10-326-186-10
27	168.5	8.2	437	4	US-10-311-623-10

28	153	7.4	141	5	US-10-471-422-4	Sequence 4, App11
29	149.5	7.3	431	4	US-10-013-173-4	Sequence 4, App11
30	149.5	7.3	431	4	US-10-150-762-4	Sequence 4, App11
31	149.5	7.3	431	4	US-10-244-821-4	Sequence 4, App11
32	149	7.2	431	5	US-10-471-422-2	Sequence 2, App11
33	140	6.8	1064	4	US-10-173-461-5	Sequence 5, App11
34	138.5	6.7	160	4	US-10-460-524-8	Sequence 2, App11
35	138.5	6.7	183	4	US-10-013-173-2	Sequence 2, App11
36	138.5	6.7	183	4	US-10-150-762-2	Sequence 2, App11
37	138.5	6.7	183	4	US-10-244-821-2	Sequence 2, App11
38	138.5	6.7	183	6	US-11-093-776-11	Sequence 11, App1
39	138.5	6.7	412	4	US-10-013-173-6	Sequence 6, App11
40	138.5	6.7	412	4	US-10-150-762-6	Sequence 6, App11
41	138.5	6.7	412	4	US-10-244-821-6	Sequence 6, App11
42	138.5	6.7	421	3	US-09-938-270B-1	Sequence 1, App11
43	138.5	6.7	423	3	US/10/013	Sequence 8, App11
44	138.5	6.7	423	4	US/10/150	Sequence 8, App11
45	138.5	6.7	423	4	US/10/244	Sequence 8, App11

ALIGNMENTS

RESULT 1

US-10-618-570-2

Sequence 2, Application US/10618570
Publication No. US20040185059A1

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RESULT 2
US-10-326-186-6

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ORGANISM: Homo sapiens
US-10-326-186-6

Query Match	50.6%	Score 1042.5;	DB 4;	Length 358;
Best Local Similarity	72.2%;	Pred. No. 3.1e-77;		
Matches 197;	Conservative 41;	Mismatches 34;	Indels 1;	Gaps 1;

Qy	MAOMDPDQOEBTDBCTSSVFKDASVALLPBPBKNGPTLOEBMSYKALITLYLV	60
Db	1 MEQMDHFHQOEBTDBCTSSVFKDASVALLPBPBKNSPTLOEBKMSFKALIALYLV	60
Qy	61 FVVLVPLIGVIAOQILKMETKNCVTGSVNA-DISPSPGKNGSEDEMRPREAVMEKSN	119
Db	61 FVVLVPLIGVIAOQILKMETKNCVSVSTVANDITOSTLGKNGDSSEBRPFQEVMEKMSN	120
Qy	120 MESRIQVLSNBEANILDAKQFONFSITTDQRFNDVLPOLNLSLSSIOEHNIIDISKL	179
Db	121 MEKRIQIILDMENANLWDTEHFONFSITTDQRFNDLILQSLSTLPSVQSHGNAIDISKL	180
Qy	180 VGLNTTVLDIOFSIETLNGRVOENAFKQOQEEKRLKEERIYNASAEISLDEKQVYLEOET	239
Db	181 ISLNTTLLDQILNIENINGKIOENTFKQOEEISLEBRVYVNSAIVAMKEEBOYHLEOEI	240
Qy	240 KGEMLKLNNTTNDRLKDMESHTLKNITLLOG	272
Db	241 KGEVKNLNTTNDRLKDMESHTLKNITLLOG	273

RESULT 3
US-10-741-600-1394

; Sequence 1394, Application US/10741600
; Publication No. US20050026169A1

```

1  APPLICANT: CARGILL, Michele et al.
2  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
3  TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
4  FILE REFERENCE: CL001499
5  CURRENT APPLICATION NUMBER: US/10/741,600
6  CURRENT FILING DATE: 2003-12-22
7  NUMBER OF SEQ ID NOS: 73997
8  SOFTWARE: PatSeq for Windows Version 4.0
9  SEQ ID NO 1394

```

ORGANISM: Homo sapiens
US-10-741-600-1394

Query Match	50.6%;	Score 1042.5;	DB 5;	length 358;
Best Local Similarity	72.2%;	Pred. No. 3.1e-77;		

Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy	1	MAQWDDPDDQOEDPDCSTCHSKYKFAKRSATALLPBPBKNGPTLOEBKSKXTALITLYLY	60
Db	1	MEQMDHFENQOEDDSCSCESVKFPDKRSMTALLPBPBKSPSOEBKSKXTALALITLYLV	60
Qy	61	FVLVLPPIGIIYAAQLLKKETKXCTGVYNA-DISESPCKGKGSBEDEMFPREAWMERSN	119
Db	61	FAVILPILGIIYAAQLLKKETKXCSYSTNANITOSTLTKGNDSEBEMFOEIVFWMHSMN	120
Qy	120	MESHITQVDSNEBANLDAKNFONSEITTDORNDVLPOLNSLSLSIOEBENITIGDISKSL	179
Db	121	MEKXIQHLLDEBANLMDTEHFOHFBMTTDORNDLLOUSTLFPSSVQSGHNAIDELSKSL	180
Qy	180	VGLNTTVLIDLOFSIETLNGRVOENAFKQOEBKRLBEERIYNASAEIKSLDEKOVYLEOET	239
Db	181	ISLMTTLLDLOLNTENLNGKIOENTFKOQOEBISKLEBRVYNVSAEIMAMKEQVHLEOET	240
Qy	240	KGEMKLLNNTNDRLKQMEHSQTLKNTTLLOG	272
Db	241	KGEYKVLNNTNDRLKQMEHSQTLRNITTLLOG	273

RESULT 4
US-10-741-600-1397
; Sequence 1397, Application US/10741600
; Publication No. US20050026169A1

```

: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele et al.
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001499
: CURRENT APPLICATION NUMBER: US/10/741.600
: CURRENT FILING DATE: 2003-12-22
: NUMBER OF SEQ ID NOS: 73997
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1397
: LENGTH: 358
: TYPE: PRN
: ORGANISM: Homo sapiens
US-10-741-600-1397

```

Query Match	50.6%	Score 1042.5;	DB 5;	length 358;
Best Local Similarity	72.2%;	Pred. NO. 3.1e-77;		
Matches 197; Conservative	41;	Mismatches 34;	Indels 1;	Gaps 1

QY	1	MAQWMDPDDQEDBDTDCSTESVYKFDARSTYALLPHAPKXGPTLQERHKSXTALITLYLY	60
Db	1	MEQMDHFNQEDBDTDCSESVYKFDARSTYALLPHAPKXSPSJOEKUKSFPALATLYLY	60
QY	61	FVVLVPIIGIYAAQLLKKETKCTYGSVVA-DISPSPEKGKGSJEDEMFREFRAVMERSN	119
Db	61	FAVILPIIGIYAAQLLKKETKCTSVSTNANDITQSLTGKGDSEBEMFQEVFMESN	120
QY	120	MESRIQVLSNDENANILDAKNFONSEITTDORNDVLFPQNLSSLTQEHENITIGDLSKL	179
Db	121	MEKRIQHLDMEANIMTDEHFONFSEMTTDDORNDLLQSTLSPSVQSGNALDELSSKL	180
QY	180	VGLNTTVLIDLQFSIETTLNGRVOENAFKOOEEMRKLEBRYLNASAEIKSLDEKQVYLEOI	239
Db	181	ISLNTTLLDLQNLNENLNGKIQENTFQOOEBISKLEBRYVNASAEIMAMKEQVHLEOI	240
QY	240	KGEKMLLNNTNDRLKDMESQTLKNTLTLOG	272
Db	241	KGEVAVLNNTNDRLKDMESQTLKNTLTLOG	273

RESULT 5
US-10-741-600-1398

; Sequence 1398, Application US/10741600
 ; Publication No. US20050026169A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CLO01499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE: 2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 1398
 LENGTH: 358
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-741-600-1398

Query Match 50.6%; Score 1042.5; DB 5; Length 358;
 Best Local Similarity 72.2%; Pred. No. 3.1e-77;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAOWDPFQOQEDPTSCSYKFDARSVTALLPFPKNGPTLOERKSYKTALITLYIIV 60
 DB 1 MEQMDHFNQOEDPTSCSYKFDARSVTALLPFPKNGPSIQERLKSFKKALLILYILV 60
 QY 61 FVLVPIIGIYVAAQLKMKETKCTVGSVNA-DISPSPGKNGSEDEMRFREAVMERMSN 119
 DB 61 FVLVPIIGIYVAAQLKMKETKCTVGSVNA-DISPSPGKNGSEDEMRFREAVMERMSN 119
 QY 120 MESRIQVSDNEANLIDAKFONFSITTDORFNDVLFOINSLSSIOEHENIGDISKSL 179
 DB 121 MEKRIQHLDEANLIDAKFONFSITTDORFNDVLFOINSLSSIOEHENIGDISKSL 180
 QY 180 VGLNTTVLDLQFSIETTLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVLEOEI 239
 DB 181 ISLNTTLLDLOINTEINLNGKIQENTFKQOEISKLEEVYVNASAIMAKKEQVLEOEI 240
 QY 240 KGEKMLNNITNDLRLKDWESHQTLRNITLLQG 272
 DB 241 KGEVVLNNITNDLRLKDWESHQTLRNITLLQG 273

RESULT 6
 US-10-741-600-1396
 Sequence 1396, Application US/10741600
 Publication No. US20050026169A1
 GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CLO01499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE: 2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 1396
 LENGTH: 388
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-741-600-1396

Query Match 50.6%; Score 1042.5; DB 5; Length 388;
 Best Local Similarity 72.2%; Pred. No. 3.5e-77;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAOWDPFQOQEDPTSCSYKFDARSVTALLPFPKNGPTLOERKSYKTALITLYIIV 60
 DB 1 MEQMDHFNQOEDPTSCSYKFDARSVTALLPFPKNGPSIQERLKSFKKALLILYILV 60
 QY 61 FVLVPIIGIYVAAQLKMKETKCTVGSVNA-DISPSPGKNGSEDEMRFREAVMERMSN 119
 DB 61 FVLVPIIGIYVAAQLKMKETKCTVGSVNA-DISPSPGKNGSEDEMRFREAVMERMSN 119
 QY 120 MESRIQVSDNEANLIDAKFONFSITTDORFNDVLFOINSLSSIOEHENIGDISKSL 179
 DB 121 MEKRIQHLDEANLIDAKFONFSITTDORFNDVLFOINSLSSIOEHENIGDISKSL 180

QY 180 VGLNTTVLDLQFSIETTLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVLEOEI 239
 DB 181 ISLNTTLLDLOINTEINLNGKIQENTFKQOEISKLEEVYVNASAIMAKKEQVLEOEI 240
 QY 240 KGEKMLNNITNDLRLKDWESHQTLRNITLLQG 272
 DB 241 KGEVVLNNITNDLRLKDWESHQTLRNITLLQG 273

RESULT 7
 US-09-782-980-19
 Sequence 19, Application US/09782980
 Patent No. US20020072089A1
 GENERAL INFORMATION:
 APPLICANT: Khodadoust, Mehran M.
 APPLICANT: Macbeth, Kyle J.
 APPLICANT: Busfield, Samantha J.
 APPLICANT: McCarthy, Sean A.
 APPLICANT: Holtzman, Douglas A.
 APPLICANT: Gu, Wei
 APPLICANT: White, David

TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND
 TITLE OF INVENTION: STMSR PROTEIN AND NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION: THEREFOR
 FILE REFERENCE: MNI-121CP
 CURRENT APPLICATION NUMBER: US/09/782,980
 CURRENT FILING DATE: 2001-02-13
 PRIOR APPLICATION NUMBER: PCT/US00/02125
 PRIOR FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: 09/448,076
 PRIOR FILING DATE: 1999-11-23
 PRIOR APPLICATION NUMBER: 09/276,400
 PRIOR FILING DATE: 1999-03-25
 PRIOR APPLICATION NUMBER: 60/117,580
 PRIOR FILING DATE: 1999-01-27
 PRIOR APPLICATION NUMBER: 09/014,195
 PRIOR FILING DATE: 1998-01-27
 PRIOR APPLICATION NUMBER: 09/014,348
 PRIOR FILING DATE: 1998-01-27
 PRIOR APPLICATION NUMBER: 09/086,892
 PRIOR FILING DATE: 1998-05-29
 PRIOR APPLICATION NUMBER: 09/296,208
 PRIOR FILING DATE: 1999-04-21
 PRIOR APPLICATION NUMBER: 09/063,950
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 09/561,381
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: 09/561,810
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: 09/087,121
 PRIOR FILING DATE: 1998-05-29
 PRIOR APPLICATION NUMBER: 09/672,721
 PRIOR FILING DATE: 2000-09-28
 PRIOR APPLICATION NUMBER: 09/049,799
 PRIOR FILING DATE: 1998-03-27
 NUMBER OF SEQ ID NOS: 176
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 19
 LENGTH: 451
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-782-980-19

Query Match 50.6%; Score 1042.5; DB 3; Length 451;
 Best Local Similarity 72.2%; Pred. No. 4.3e-77;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAOWDPFQOQEDPTSCSYKFDARSVTALLPFPKNGPTLOERKSYKTALITLYIIV 60
 DB 1 MEQMDHFNQOEDPTSCSYKFDARSVTALLPFPKNGPSIQERLKSFKKALLILYILV 60
 QY 61 FVLVPIIGIYVAAQLKMKETKCTVGSVNA-DISPSPGKNGSEDEMRFREAVMERMSN 119

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Db 61 FAVLIPILIGIVAAQLMKETKNCVSSTNANDITQSLTGKNDSEEMRFOEVMEMHSN 120
Qy 120 MESIOYLSNEANLDAKNFONFSITTDORFNDVLPLNLSLSIOEHENIIGDISKSL 179
Db 121 MEKIQHLDMEANLMDTEHFONFSMTTDORFNDILQLSTLFSVQGHGAIDBEISKSL 180
Qy 180 VGLNTTVLADLOFSIETLNGRVOENAFKQOEEMRKLEERINYASAEIKSLDEKQVYLEOEI 239
Db 181 ISLNTTLLDLOLNTENLNGKIQENTFKQOEISKLEERVYVNSAEIYAMKEQVHLEOEI 240
Qy 240 KGEVKLVNNTNDRLKDMWHSQTLRNITLLIOG 272
Db 241 KGEVKLVNNTNDRLKDMWHSQTLRNITLLIOG 273

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RESULT 8
US-09-909-743-10
Sequence 10, Application US/09909743
Patent No. US20020151007A1
GENERAL INFORMATION:
APPLICANT: Khodadoust, Mehran et al.
TITLE OF INVENTION: METHODS OF USE OF A NOVEL LYSYL OXIDASE-RELATED
FILE REFERENCE: MN1-073CP
CURRENT FILING DATE: 2001-07-20
CURRENT APPLICATION NUMBER: US/09/909,743
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/448,076
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/276,400
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 451
TYPE: PRT
ORGANISM: Homo sapiens
US-09-909-743-10

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Query Match 50.6%; Score 1042.5; DB 3; Length 451;
Best Local Similarity 72.2%; Pred. No. 4,3e-77;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MAQWDDPDDQOEDTDSCTESVYKFDARSVTALLPFPKNGPTLOERMKSYKTALLITLYLIY 60
Db 1 MEQWDHFNQOEDTDSCTESVYKFDARSMTALLPFPKNSPQLQKLSFKKALLALYLIY 60
Qy 61 FVILVPIIGIYVAAQLMKETKNCVSVNA-DISPSPEKNGSGEDEMRFREAVEMKSN 119
Db 61 FAVLIPILIGIVAAQLMKETKNCVSSTNANDITQSLTGKNDSEEMRFOEVMEMHSN 120
Qy 120 MESIOYLSNEANLDAKNFONFSITTDORFNDVLPLNLSLSIOEHENIIGDISKSL 179
Db 121 MEKIQHLDMEANLMDTEHFONFSMTTDORFNDILQLSTLFSVQGHGAIDBEISKSL 180
Qy 180 VGLNTTVLADLOFSIETLNGRVOENAFKQOEEMRKLEERINYASAEIKSLDEKQVYLEOEI 239
Db 181 ISLNTTLLDLOLNTENLNGKIQENTFKQOEISKLEERVYVNSAEIYAMKEQVHLEOEI 240
Qy 240 KGEVKLVNNTNDRLKDMWHSQTLRNITLLIOG 272
Db 241 KGEVKLVNNTNDRLKDMWHSQTLRNITLLIOG 273

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RESULT 9
US-10-426-262-2
Sequence 2, Application US/10426262
Publication No. US20040018521A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianfeng
APPLICANT: Meyers, Deborah
APPLICANT: Zheng, Sigun
APPLICANT: Walsh, Patrick C.

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APPLICANT: Isaacs, William B.
APPLICANT: Bleeker, Eugene
TITLE OF INVENTION: MUTATIONS IN THE MACROPHAGE SCAVENGER RECEPTOR 1 GENE ALTER RISK
FILE REFERENCE: 9151-23
CURRENT APPLICATION NUMBER: US/10/426,262
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 451
TYPE: PRT
ORGANISM: Homo sapiens
US-10-426-262-2

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Query Match 50.6%; Score 1042.5; DB 4; Length 451;
Best Local Similarity 72.2%; Pred. No. 4,3e-77;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MAQWDDPDDQOEDTDSCTESVYKFDARSVTALLPFPKNGPTLOERMKSYKTALLITLYLIY 60
Db 1 MEQWDHFNQOEDTDSCTESVYKFDARSMTALLPFPKNSPQLQKLSFKKALLALYLIY 60
Qy 61 FVILVPIIGIYVAAQLMKETKNCVSVNA-DISPSPEKNGSGEDEMRFREAVEMKSN 119
Db 61 FAVLIPILIGIVAAQLMKETKNCVSSTNANDITQSLTGKNDSEEMRFOEVMEMHSN 120
Qy 120 MESIOYLSNEANLDAKNFONFSITTDORFNDVLPLNLSLSIOEHENIIGDISKSL 179
Db 121 MEKIQHLDMEANLMDTEHFONFSMTTDORFNDILQLSTLFSVQGHGAIDBEISKSL 180
Qy 180 VGLNTTVLADLOFSIETLNGRVOENAFKQOEEMRKLEERINYASAEIKSLDEKQVYLEOEI 239
Db 181 ISLNTTLLDLOLNTENLNGKIQENTFKQOEISKLEERVYVNSAEIYAMKEQVHLEOEI 240
Qy 240 KGEVKLVNNTNDRLKDMWHSQTLRNITLLIOG 272
Db 241 KGEVKLVNNTNDRLKDMWHSQTLRNITLLIOG 273

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RESULT 10
US-10-423-543-80
Sequence 80, Application US/10423543
Publication No. US20040058355A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Libermann, Rosana K.
APPLICANT: Hunter, John J.
APPLICANT: Meyers, Rachel E.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Curtiss, Rory A.J.
APPLICANT: Olandt, Peter J.
APPLICANT: Tsai, Fong-Ying
APPLICANT: Galvin, Katherine M.
APPLICANT: Chun, Miyoung
APPLICANT: Williamson, Mark J.
APPLICANT: Silos-Santiago, Immaculada
APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: NOVEL 21910, 56634, 55053, 2504, 15977,
TITLE OF INVENTION: 14760, 33217, 21967, 11983, m1983, 38555 OR 593 MOLECULES
TITLE OF INVENTION: 18610, 33217, 21967, 11983, m1983, 38555 OR 593 MOLECULES
FILE REFERENCE: MP103-023ONMIN
CURRENT APPLICATION NUMBER: US/10/423,543
CURRENT FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 10/278,036
PRIOR FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: US 09/711,216
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/205,447
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 10/012,055
PRIOR FILING DATE: 2001-11-13

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PRIOR APPLICATION NUMBER: US 60/248,325
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 10/003,690
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/248,893
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 09/797,039
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/186,061
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: US 10/217,168
PRIOR FILING DATE: 2002-08-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 119
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 80
LENGTH: 451
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-423-543-80

Query Match 50.6%; Score 1042.5; DB 4; Length 451;
Best Local Similarity 72.2%; Pred. No. 4.3e-77;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDPDQOEDTSCSSEVYKFDARSVTALLPFPKNGPTLOEEMKSKYKTLITLYLV 60
DB 1 MEQWDFHNOEDTSCSSEVYKFDARSVTALLPFPKNGPTLOEEMKSKYKTLITLYLV 60
QY 61 FVLVPIIGIYVAQLLKKETKNCVSVNA-DISPSPEKNGSDEMRPREAVEMRSN 119
DB 61 FVLVPIIGIYVAQLLKKETKNCVSVSTNANDITQSLTGKNDSEEMRFOEVFMEHNSN 120
QY 120 MESRQYSDNEANLLDAKNFONFSTTDDQRPNDVLPQNLSSLOEHENITIGDISKL 179
DB 121 MEKRIOHILDEANIMDEHPNFMSITDQRPNDILQLSTFSSVOGNAIDISKSL 180
QY 180 VGLNTTVLDLOFSEITLNGRVOENAFKQOEEMKLEERYNVAASIKSLDEKQVLEOEI 239
DB 181 ISLNTTLDLQNLINLNGKIOENTFKQOEESKLEERYNVAASIMAKEQVLEOEI 240
QY 240 KGEMLNNITNDLRLKQWESQTLKNTLLQG 272
DB 241 KGEVAVLNNITNDLRLKQWESQTLKNTLLQG 273

RESULT 11
US-10-806-018-19
Sequence 19, Application US/10806018
Publication No. US20040176296A1
GENERAL INFORMATION:
APPLICANT: Knodadoust, Mehran M.
APPLICANT: Macbeth, Kyle J.
APPLICANT: Busfield, Samantha J.
APPLICANT: McCarthy, Sean A.
APPLICANT: Holzman, Douglas A.
APPLICANT: Gu, Wei
APPLICANT: White, David
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND
TITLE OF INVENTION: STMS PROTEIN AND NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: MNT-121CP
CURRENT APPLICATION NUMBER: US/10/806,018
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US/09/782,980
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: PCT/US00/02125
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 09/448,076
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: 09/276,400
PRIOR FILING DATE: 1999-03-25

PRIOR APPLICATION NUMBER: 60/117,580
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 09/014,195
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: 09/014,348
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: 09/086,892
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 09/296,208
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 09/063,950
PRIOR FILING DATE: 1998-04-21
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 176
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 451
TYPE: PRT
ORGANISM: Homo sapiens
US-10-806-018-19

Query Match 50.6%; Score 1042.5; DB 4; Length 451;
Best Local Similarity 72.2%; Pred. No. 4.3e-77;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDPDQOEDTSCSSEVYKFDARSVTALLPFPKNGPTLOEEMKSKYKTLITLYLV 60
DB 1 MEQWDFHNOEDTSCSSEVYKFDARSVTALLPFPKNGPTLOEEMKSKYKTLITLYLV 60
QY 61 FVLVPIIGIYVAQLLKKETKNCVSVNA-DISPSPEKNGSDEMRPREAVEMRSN 119
DB 61 FVLVPIIGIYVAQLLKKETKNCVSVSTNANDITQSLTGKNDSEEMRFOEVFMEHNSN 120
QY 120 MESRQYSDNEANLLDAKNFONFSTTDDQRPNDVLPQNLSSLOEHENITIGDISKL 179
DB 121 MEKRIOHILDEANIMDEHPNFMSITDQRPNDILQLSTFSSVOGNAIDISKSL 180
QY 180 VGLNTTVLDLOFSEITLNGRVOENAFKQOEEMKLEERYNVAASIKSLDEKQVLEOEI 239
DB 181 ISLNTTLDLQNLINLNGKIOENTFKQOEESKLEERYNVAASIMAKEQVLEOEI 240
QY 240 KGEMLNNITNDLRLKQWESQTLKNTLLQG 272
DB 241 KGEVAVLNNITNDLRLKQWESQTLKNTLLQG 273

RESULT 12
US-10-741-600-1395
Sequence 1395, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1395
LENGTH: 451
TYPE: PRT
ORGANISM: Homo sapiens
US-10-741-600-1395

Query Match 50.6%; Score 1042.5; DB 5; Length 451;
Best Local Similarity 72.2%; Pred. No. 4.3e-77;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDPDQOEDTSCSSEVYKFDARSVTALLPFPKNGPTLOEEMKSKYKTLITLYLV 60
DB 1 MEQWDFHNOEDTSCSSEVYKFDARSVTALLPFPKNGPTLOEEMKSKYKTLITLYLV 60

Query Match	38.9%	Score 801;	DB 3;	Length 458,
Best Local Similarity	59.4%;	Pred. No. 3.5e-57;		
Matches 158; Conservative	46;	Mismatches 60;	Indels 2;	Gaps 2

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Qy      8 PDQEDTDSCTESVYKFDARSVTALL.PPHKNGPTLOERBMSKYKATLITLYLVFVVLPI 67
      13 PHEREDADCSSESXVFDARSMATSLPHSTKNGPSVQETLKSKKALILALYLVFVVLPIV 72
Qy      68 IGIYAQQLKMETKNCCTVGSVN-ADISPEGKNGSEDEMFRFAVNERMSMESRIQY 126
      73 VGIYVAQQLNEMKNCCLVCSRTSDTSGPMEKENTSNVEMRF-TIIMAHMKDMEERIQS 131
Db      127 LSDNEANLIDAKNFONFSITTDQRNDVLFQNLSSLSIQEHENIIGDISKSLVGLNTTV 186
      132 ISNSKADLIDTGRFONFSMATDQRLNDILLQNLSSLSIQEHGNSLDAISKSLQSLMNTL 191
Qy      167 LDLOPSIFTLNGRVOENAFKOOEERKLEERYLYNSAETKSLDEKQVYVLEQIKGEMKLL 246
      192 LDVQHTETLHVRVVESTAKQOEDISKLEERYKYSAEVSQVKEQAHVEQKQEVRL 251
Db      247 NNITNDLRKQWHSQTLKNITLLOG 272
      252 NNITNDLRKQWHSQTLKNITFIQ 277

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RESULT 15
US-10-806-018-126

Sequence 126, Application US/10806018
Publication No. US20040176296A1

GENERAL INFORMATION:

APPLICANT: Knodadouc, Mehrian M.

APPLICANT: Macbeth, Kyle J.

APPLICANT: Busfield, Samantha J.

APPLICANT: McCarthy, Sean A.

APPLICANT: Holtzman, Douglas A.

APPLICANT: Gu, Wei

APPLICANT: White, David

APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, IRSG, AND

TITLE OF INVENTION: STMSI PROTEIN AND NUCLEIC ACID MOLECULES AND USES

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: MNT-121CP

CURRENT APPLICATION NUMBER: US/10/806, 018

PRIOR FILING DATE: 2004-03-22

PRIOR APPLICATION NUMBER: US/09/782, 980

PRIOR FILING DATE: 2001-02-13

PRIOR APPLICATION NUMBER: PCT/US00/02125

PRIOR FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: 09/448, 076

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: 09/276, 400

PRIOR FILING DATE: 1999-03-25

PRIOR APPLICATION NUMBER: 60/117, 580

PRIOR FILING DATE: 1999-01-27

PRIOR APPLICATION NUMBER: 09/014, 195

PRIOR FILING DATE: 1998-01-27

PRIOR APPLICATION NUMBER: 09/014, 348

PRIOR FILING DATE: 1998-01-27

PRIOR APPLICATION NUMBER: 09/086, 892

PRIOR FILING DATE: 1998-05-29

PRIOR APPLICATION NUMBER: 09/296, 208

PRIOR FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: 09/063, 950

PRIOR FILING DATE: 1998-04-21

Remaining prior Application data removed - See file Wrapper or PALM.

NUMBER OF SEQ ID NOS: 176

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 126

LENGTH: 458

TYPE: PRT

ORGANISM: Mus Musculus

US-10-806-018-126

Query Match

Best Local Similarity 59.4%;

Matches 158; Conservative 46; Mismatches 60; Indels 2; Gaps 2;

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Qy      8 PDQEDTDSCTESVYKFDARSVTALL.PPHKNGPTLOERBMSKYKATLITLYLVFVVLPI 67
      13 PHEREDADCSSESXVFDARSMATSLPHSTKNGPSVQETLKSKKALILALYLVFVVLPIV 72
Qy      68 IGIYAQQLKMETKNCCTVGSVN-ADISPEGKNGSEDEMFRFAVNERMSMESRIQY 126
      73 VGIYVAQQLNEMKNCCLVCSRTSDTSGPMEKENTSNVEMRF-TIIMAHMKDMEERIQS 131
Db      127 LSDNEANLIDAKNFONFSITTDQRNDVLFQNLSSLSIQEHENIIGDISKSLVGLNTTV 186
      132 ISNSKADLIDTGRFONFSMATDQRLNDILLQNLSSLSIQEHGNSLDAISKSLQSLMNTL 191
Qy      167 LDLOPSIFTLNGRVOENAFKOOEERKLEERYLYNSAETKSLDEKQVYVLEQIKGEMKLL 246
      192 LDVQHTETLHVRVVESTAKQOEDISKLEERYKYSAEVSQVKEQAHVEQKQEVRL 251
Db      247 NNITNDLRKQWHSQTLKNITLLOG 272
      252 NNITNDLRKQWHSQTLKNITFIQ 277

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Search completed: February 16, 2006, 17:09:31
Job time : 167 secs

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

- Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
- Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 17:06:52 ; Search time 18 Seconds

(without alignments)
315.881 Million cell updates/sec

Title: US-10-618-570-2

Sequence: 1 MAQMDPDPQOEEDTDSCTES.....DKMTRVCINIFTRLRQKE 400

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgcn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /cgcn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
3: /cgcn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
4: /cgcn2_6/ptodata/1/pubpaa/ECT_NEW_PUB pep.*
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7: /cgcn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
8: /cgcn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1042.5	50.6	358	US-10-995-561-885	Sequence 885, App
2	1042.5	50.6	358	US-10-995-561-888	Sequence 888, App
3	1042.5	50.6	358	US-10-995-561-889	Sequence 889, App
4	1042.5	50.6	388	US-10-995-561-887	Sequence 887, App
5	1042.5	50.6	451	US-10-995-561-886	Sequence 886, App
6	138.5	6.7	421	US-10-673-781-1	Sequence 1, Appli
7	135.5	6.6	270	US-11-123-696A-3	Sequence 3, Appli
8	129	6.3	1404	US-10-878-556A-159	Sequence 159, App
9	125.5	6.1	2665	US-11-124-368A-214	Sequence 214, App
10	125.5	6.1	2668	US-11-124-368A-215	Sequence 215, App
11	122.5	5.9	5024	US-10-793-626-296A	Sequence 296A, App
12	120	5.8	885	US-10-793-626-1660	Sequence 1660, App
13	115.5	5.6	492	US-11-152-697-2	Sequence 2, Appli
14	115.5	5.6	539	US-11-152-697-5	Sequence 5, Appli
15	110.5	5.4	1095	US-10-793-626-315A	Sequence 315A, App
16	109.5	5.3	1266	US-10-995-561-665	Sequence 665, App
17	109.5	5.3	1652	US-10-995-561-663	Sequence 663, App
18	109.5	5.3	1938	US-10-995-561-661	Sequence 661, App
19	109.5	5.3	1938	US-10-995-561-662	Sequence 662, App
20	109.5	5.3	1954	US-10-995-561-660	Sequence 660, App
21	109.5	5.3	1972	US-10-995-561-664	Sequence 664, App
22	109.5	5.3	1972	US-10-995-561-666	Sequence 666, App
23	107.5	5.2	489	US-10-537-075-11	Sequence 11, Appli
24	106.5	5.2	496	US-11-067-121-12	Sequence 12, Appli
25	106.5	5.2	496	US-11-129-076-7	Sequence 7, Appli

26	106	5.1	373	US-11-072-512-1995	Sequence 1995, App
27	105.5	5.1	1562	US-11-052-554A-211	Sequence 211, App
28	105.5	5.1	1786	US-11-196-400-3	Sequence 3, Appli
29	104.5	5.1	1126	US-10-485-517-248	Sequence 248, App
30	104	5.1	955	US-11-052-554A-179	Sequence 179, App
31	104	5.1	1189	US-11-074-176-134	Sequence 134, App
32	102.5	5.0	706	US-10-485-517-146	Sequence 146, App
33	100.5	4.9	860	US-11-019-711-59	Sequence 59, Appli
34	100.5	4.9	862	US-11-128-420-11	Sequence 11, Appli
35	100.5	4.9	862	US-11-007-428-2	Sequence 2, Appli
36	100.5	4.9	862	US-11-183-294-16	Sequence 16, Appli
37	100	4.9	547	US-11-052-554A-285	Sequence 285, App
38	100	4.9	700	US-11-196-475-66	Sequence 66, Appli
39	99.5	4.8	335	US-10-453-372-426	Sequence 426, App
40	99.5	4.8	335	US-10-453-372-428	Sequence 428, App
41	99.5	4.8	446	US-11-098-686-10239	Sequence 10239, A
42	99.5	4.8	1538	US-10-995-561-772	Sequence 772, App
43	99.5	4.8	2107	US-10-995-561-827	Sequence 827, App
44	99.5	4.8	2480	US-10-995-561-825	Sequence 825, App
45	99.5	4.8	3116	US-10-995-561-826	Sequence 826, App

ALIGNMENTS

RESULT 1	US-10-995-561-885	Application US/10995561
Sequence 885, Application US/10995561	Publication No. US20050272054A1	GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.	TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH	TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF	FILE REFERENCE: CL001559	CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24	NUMBER OF SEQ ID NOS: 85702	SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 885	SEQ ID NO 885	LENGTH: 358
TYPE: PRT	ORGANISM: Homo sapiens	US-10-995-561-885
Query Match	50.6%; Score 1042.5; DB 6; Length 358;	Best Local Similarity 72.2%; Pred. No. 8.9e-67;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;		
QY	1 MAQMDPDPQOEEDTDSCTESVVFEDARSVTALPPHKKGPPTLOEEMKSYKTLITLYLV 60	
DB	1 MEQWHFHQOEEDTDSCTESVVFEDARSVTALPPHKKGPPTLOEEMKSYKTLITLYLV 60	
QY	61 FVVLVPIIGIIVAAQLLKKETKCTVGSVNA-DISPSPEKGGSGSEDMRFREAVMERMSN 119	
DB	61 FAVLIPILGIVAAQLLKKETKCTVGSVNA-DISPSPEKGGSGSEDMRFREAVMERMSN 120	
QY	120 MESRIQYISDNEANLIDAKNFONFISITTDORNDVLFQNLSSLSIOEHENIIGDISKL 179	
DB	121 MEKRIOHILIDMEANLIDTEHPONFMTTDORNDVILQSLTFSSVOGNAIDETISKL 180	
QY	180 VGLNTTVLDIOSIFETLGRVOENAFKQOEERKJLEERLYNNAEIKSLDEQVYLEORI 239	
DB	181 ISLNTTLLDLQNLINENKGIQENFKQOEERKJLEERLYNNAEIKSLDEQVYLEORI 240	
QY	240 KGEMLLNNTTNDLRLKQWEHSQTLKNITLLQG 272	
DB	241 KGEVAVANNITNDLRLKQWEHSQTLKNITLLIG 273	
RESULT 2	US-10-995-561-888	Application US/10995561
Sequence 888, Application US/10995561		

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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 888
LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-888

Query Match      50.6%; Score 1042.5; DB 6; Length 358;
Best Local Similarity 72.2%; Pred. No. 8.9e-67;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Cy 1 MAQWDPDQOEDTDSCTESYKFDARSVTALLPBPKNKGPITLOERMSYKTALITLYIIV 60
Db 1 MEQWDHFNQOEDTDSCTESYKFDARSMTALLPBPKNKSPSLQEKLSFKKALIALYIIV 60

Cy 61 FVLVPIIGIYAAQLKMKETKCTVGSYNA-DISPSPEKNGSGEDENRFEAVMERMSN 119
Db 61 FAVLIPILGIYAAQLKMKETKCTVGSYNA-DISPSPEKNGSGEDENRFEAVMERMSN 120

Cy 120 MESRIQYLSDEANILDAKNFONSITTDQRFNVLFOPLNSLSIOEHENIGDISKSL 179
Db 120 MESRIQYLSDEANILDAKNFONSITTDQRFNVLFOPLNSLSIOEHENIGDISKSL 179

Cy 121 MEKRIQHLIDMEANILMDTEHFQNFMTTDQRFNVLFOPLNSLSIOEHENIGDISKSL 180
Db 121 MEKRIQHLIDMEANILMDTEHFQNFMTTDQRFNVLFOPLNSLSIOEHENIGDISKSL 180

Cy 180 VGLNTTVLDLOFSIETLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVYLBEOI 239
Db 180 VGLNTTVLDLOFSIETLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVYLBEOI 239

Cy 240 KGEVKLVNNTITNDRLKDMESHSQTLRNITLLIOG 272
Db 240 KGEVKLVNNTITNDRLKDMESHSQTLRNITLLIOG 273

RESULT 3
US-10-995-561-889
Sequence 889, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 889
LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-889

Query Match      50.6%; Score 1042.5; DB 6; Length 358;
Best Local Similarity 72.2%; Pred. No. 8.9e-67;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Cy 1 MAQWDPDQOEDTDSCTESYKFDARSVTALLPBPKNKGPITLOERMSYKTALITLYIIV 60
Db 1 MEQWDHFNQOEDTDSCTESYKFDARSMTALLPBPKNKSPSLQEKLSFKKALIALYIIV 60

Cy 61 FVLVPIIGIYAAQLKMKETKCTVGSYNA-DISPSPEKNGSGEDENRFEAVMERMSN 119
Db 61 FAVLIPILGIYAAQLKMKETKCTVGSYNA-DISPSPEKNGSGEDENRFEAVMERMSN 120

Cy 120 MESRIQYLSDEANILDAKNFONSITTDQRFNVLFOPLNSLSIOEHENIGDISKSL 179
Db 120 MESRIQYLSDEANILDAKNFONSITTDQRFNVLFOPLNSLSIOEHENIGDISKSL 179

Cy 121 MEKRIQHLIDMEANILMDTEHFQNFMTTDQRFNVLFOPLNSLSIOEHENIGDISKSL 180
Db 121 MEKRIQHLIDMEANILMDTEHFQNFMTTDQRFNVLFOPLNSLSIOEHENIGDISKSL 180

Cy 180 VGLNTTVLDLOFSIETLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVYLBEOI 239
Db 180 VGLNTTVLDLOFSIETLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVYLBEOI 239

Cy 240 KGEVKLVNNTITNDRLKDMESHSQTLRNITLLIOG 272
Db 240 KGEVKLVNNTITNDRLKDMESHSQTLRNITLLIOG 273

RESULT 4
US-10-995-561-887
Sequence 887, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 887
LENGTH: 388
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-887

Query Match      50.6%; Score 1042.5; DB 6; Length 388;
Best Local Similarity 72.2%; Pred. No. 9.9e-67;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Cy 1 MAQWDPDQOEDTDSCTESYKFDARSVTALLPBPKNKGPITLOERMSYKTALITLYIIV 60
Db 1 MEQWDHFNQOEDTDSCTESYKFDARSMTALLPBPKNKSPSLQEKLSFKKALIALYIIV 60

Cy 61 FVLVPIIGIYAAQLKMKETKCTVGSYNA-DISPSPEKNGSGEDENRFEAVMERMSN 119
Db 61 FAVLIPILGIYAAQLKMKETKCTVGSYNA-DISPSPEKNGSGEDENRFEAVMERMSN 120

Cy 120 MESRIQYLSDEANILDAKNFONSITTDQRFNVLFOPLNSLSIOEHENIGDISKSL 179
Db 120 MESRIQYLSDEANILDAKNFONSITTDQRFNVLFOPLNSLSIOEHENIGDISKSL 179

Cy 121 MEKRIQHLIDMEANILMDTEHFQNFMTTDQRFNVLFOPLNSLSIOEHENIGDISKSL 180
Db 121 MEKRIQHLIDMEANILMDTEHFQNFMTTDQRFNVLFOPLNSLSIOEHENIGDISKSL 180

Cy 180 VGLNTTVLDLOFSIETLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVYLBEOI 239
Db 180 VGLNTTVLDLOFSIETLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVYLBEOI 239

Cy 240 KGEVKLVNNTITNDRLKDMESHSQTLRNITLLIOG 272
Db 240 KGEVKLVNNTITNDRLKDMESHSQTLRNITLLIOG 273

RESULT 5
US-10-995-561-886
Sequence 886, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
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120 MESRIQYLSDEANILDAKNFONSITTDQRFNVLFOPLNSLSIOEHENIGDISKSL 179
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180 VGLNTTVLDLOFSIETLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVYLBEOI 239
181 ISLNTTLLDLOLNTENLNKIQENTPFKQOEBISKLEERVYVNSAEIWMKEQVYLBEOI 240

Cy 240 KGEVKLVNNTITNDRLKDMESHSQTLRNITLLIOG 272
Db 241 KGEVKLVNNTITNDRLKDMESHSQTLRNITLLIOG 273

RESULT 4
US-10-995-561-887
Sequence 887, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 887
LENGTH: 388
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-887

Query Match      50.6%; Score 1042.5; DB 6; Length 388;
Best Local Similarity 72.2%; Pred. No. 9.9e-67;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Cy 1 MAQWDPDQOEDTDSCTESYKFDARSVTALLPBPKNKGPITLOERMSYKTALITLYIIV 60
Db 1 MEQWDHFNQOEDTDSCTESYKFDARSMTALLPBPKNKSPSLQEKLSFKKALIALYIIV 60

Cy 61 FVLVPIIGIYAAQLKMKETKCTVGSYNA-DISPSPEKNGSGEDENRFEAVMERMSN 119
Db 61 FAVLIPILGIYAAQLKMKETKCTVGSYNA-DISPSPEKNGSGEDENRFEAVMERMSN 120

Cy 120 MESRIQYLSDEANILDAKNFONSITTDQRFNVLFOPLNSLSIOEHENIGDISKSL 179
Db 120 MESRIQYLSDEANILDAKNFONSITTDQRFNVLFOPLNSLSIOEHENIGDISKSL 179

Cy 121 MEKRIQHLIDMEANILMDTEHFQNFMTTDQRFNVLFOPLNSLSIOEHENIGDISKSL 180
Db 121 MEKRIQHLIDMEANILMDTEHFQNFMTTDQRFNVLFOPLNSLSIOEHENIGDISKSL 180

Cy 180 VGLNTTVLDLOFSIETLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVYLBEOI 239
Db 180 VGLNTTVLDLOFSIETLNGRVOENAFKQOEBMRKLEERIYNASAEIKSLDEKQVYLBEOI 239

Cy 240 KGEVKLVNNTITNDRLKDMESHSQTLRNITLLIOG 272
Db 241 KGEVKLVNNTITNDRLKDMESHSQTLRNITLLIOG 273

RESULT 5
US-10-995-561-886
Sequence 886, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 886
 LENGTH: 451
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-995-561-886

Query Match 50.6%; Score 1042.5; DB 6; Length 451;
 Best Local Similarity 72.2%; Pred. No. 1.2e-66;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDPDQOEDTSCIESVFKDARSVTALLPPHPKNGPTLOERNKSYKTLITLYIV 60
 DB 1 MEQWDFHNOQEDTSCIESVFKDARSVTALLPPHPKNSPSIQEKIKSPKALILYLYIV 60
 QY 61 FVYVPIIGIYVAOLKXETKCTGVSVA--DISPSEKNGSGDEMPREAVWERN 119
 DB 61 FAVLIPLIGIYVAOLKXETKCTGVSVA--DISPSEKNGSGDEMPREAVWERN 120
 QY 120 MESRIQYLDSEANLLDAKQNFISITTDQRENDVLFQNLSSIOEHENIIGDISKL 179
 DB 121 MEKRIQYLDSEANLLDAKQNFISITTDQRENDVLFQNLSSIOEHENIIGDISKL 180
 QY 180 VGLNTTVLDQFSITLNGRVOENAFKQOENRKLERYNASEIKSIDKQVYLEDEI 239
 DB 181 ISLNTTLLDLQNLINENLNGKIQENTFKQOERISKLEERYVNASAEIMAKKEQVHLEGEI 240
 QY 240 KGEMLNNITNDLRLKQWESQTLKNITLLQG 272
 DB 241 KGEVKNNTITNDLRLKQWESQTLKNITLLQG 273

RESULT 6
 US-10-673-781-1
 Sequence 1, Application US/10673781
 Publication No. US20050260689A1

GENERAL INFORMATION:
 APPLICANT: Olmwei Shi
 TITLE OF INVENTION: Differential Immunoassay
 FILE REFERENCE: 1112-1-080N
 CURRENT APPLICATION NUMBER: US/10/673,781
 CURRENT FILING DATE: 2003-09-29
 PRIOR APPLICATION NUMBER: US/09/938,270B
 PRIOR FILING DATE: 2001-08-23
 PRIOR APPLICATION NUMBER: US 60/227,536
 PRIOR FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: US 60/292,497
 PRIOR FILING DATE: 2001-05-21
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PaetSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 421
 TYPE: PRT
 ORGANISM: homoeaplen
 US-10-673-781-1

Query Match 6.7%; Score 138.5; DB 6; Length 421;
 Best Local Similarity 33.1%; Pred. No. 0.0091;
 Matches 43; Conservative 18; Mismatches 56; Indels 13; Gaps 7;

QY 273 ARKSLTGKMTNDGSMNTIGAVNSRGEFTGYITAV-TATSNIKESPLHGTONINKR 331
 DB 13 AAEAGITGWTYNQDSTFIYVA-GADGALTGYBSAVGASRYVLTGRYDSAPATDQSG 71
 QY 332 TOPFTGFTYVWK---FSESTVFTGQCFIDRNGKEV-LKTMWLLRSSVNDIGDDWKATR 386
 DB 72 T--ALGWTYVAMKNNRYNAHSATWISQYV---GGAERINTQWLLTSGTTE-ANAMKSTYL 125
 QY 387 VGINFTRLR 396
 DB 126 VGHDTFTKVK 135

RESULT 7

US-11-123-696A-3
 Sequence 3, Application US/11123696A
 Publication No. US20060024766A1
 GENERAL INFORMATION:
 APPLICANT: ATWELL, JOHN LESLIE
 APPLICANT: DEVINE, PETER LEONARD
 APPLICANT: KORTY, ALEXANDER ANDREW
 APPLICANT: PERRY, GILLIAN WENDY
 APPLICANT: BUNDESEN, PETER GREGORY
 TITLE OF INVENTION: BIFUNCTIONAL MOLECULES
 FILE REFERENCE: 674537-2001.1
 CURRENT APPLICATION NUMBER: US/11/123,696A
 CURRENT FILING DATE: 2005-05-05
 PRIOR APPLICATION NUMBER: 09/581,924
 PRIOR FILING DATE: 2000-06-19
 PRIOR APPLICATION NUMBER: PCT/AU98/01076
 PRIOR FILING DATE: 1998-12-24
 PRIOR APPLICATION NUMBER: AU PP1110
 PRIOR FILING DATE: 1997-12-24
 PRIOR APPLICATION NUMBER: AU PP5176
 PRIOR FILING DATE: 1998-08-11
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: Patencin Ver. 3.3

SEQ ID NO 3
 LENGTH: 270
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: construct of S. avidin and human immunoglobulin
 US-11-123-696A-3

Query Match 6.6%; Score 135.5; DB 7; Length 270;
 Best Local Similarity 32.8%; Pred. No. 0.0082;
 Matches 42; Conservative 18; Mismatches 55; Indels 13; Gaps 7;

QY 275 KCSLTGKMTNDGSMNTIGAVNSRGEFTGYITAV-TATSNIKESPLHGTONINKRQ 333
 DB 23 EAGITGWTYNQDSTFIYVA-GADGALTGYBSAVGASRYVLTGRYDSAPATDQSGT- 80
 QY 334 PFTGFTYVWK---FSESTVFTGQCFIDRNGKEV-LKTMWLLRSSVNDIGDDWKATR 388
 DB 81 -ALGWTYVAMKNNRYNAHSATWISQYV---GGAERINTQWLLTSGTTE-ANAMKSTYL 135
 QY 389 INIFTRLR 396
 DB 136 HDTFTKVK 143

RESULT 8
 US-10-878-556A-169

Sequence 169, Application US/10878556A
 Publication No. US20050266399A1
 GENERAL INFORMATION:
 APPLICANT: Hoffmann La-Roche Inc.
 TITLE OF INVENTION: HCV regulated protein expression
 FILE REFERENCE: 21762
 CURRENT APPLICATION NUMBER: US/10/878,556A
 CURRENT FILING DATE: 2004-06-28
 NUMBER OF SEQ ID NOS: 199
 SOFTWARE: Patencin version 3.1
 SEQ ID NO 169
 LENGTH: 1404
 TYPE: PRT
 ORGANISM: Homo sapiens
 DATABASE ACCESSION NUMBER: humangp/chr12-q14221
 DATABASE ENTRY DATE: 2003-04-22
 US-10-878-556A-169

Query Match 6.3%; Score 129; DB 6; Length 1404;
 Best Local Similarity 21.5%; Pred. No. 0.21;
 Matches 98; Conservative 69; Mismatches 175; Indels 114; Gaps 18;

[illegible]

```

RESULT 9
US-11-124-368A-214
; Sequence 214, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: C1001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; PRIORITY FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIORITY FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIORITY FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 2112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 2665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-214

```

Query Match	6.1%;	Score 125.5;	DB 7;	Length 2665;
Best Local Similarity	20.1%;	Pred. No. 0.87;		
Matches 92;	Conservative 90;	Mismatches 157;	Indels 119;	Gaps 20;

```
QY      3 QMDFPDQOEEDTSCSTSVKFDARVTLALPHPNKGFTLOERMSXYTALTLYLVIVF 62
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      888 EMEOKEOLERNRDSLTQTVREKTLITFKLQOTLEEVTLTOEKDMLQOLESL----- 941
QY      63 VLVPILGVAAQLTKWETKNCTGVSVMNDISPSPEKGSNDEMRPREAV---MERMSN 119
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      942 -----QIREDQLKSIDIHTVNAMID-TQQLRNALRESLKQHOFETINTLSKISE 989
QY      120 MESRIQVLSDNEMANL-----LDANKFNFSITTDQRNDVLFQUNLLS 163
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```

Db      990 EVSNINHEENTGTXKDFEQKRWGIDDKQDLKANNQ--TLTADVKNONEIIEQGRKFS 1047

QY      164 SIOEHENITGDISKSLVG---LNTVLDLPSTIE-TLNG---RVGENAKQOE----- 210
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1048 LIOR-KNELQOMLESVIAEKEQOLT--DLKENEMTENGEBELRLGDELKKOEIVAQ 1103
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      211 -----MRKLEBRYNASAEIKSLDEKQVYLEBOEIKGEMKLIN---NI 249
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db      1104 EKNAHAIKKEGELSRTCDRLAEVEBRLKAEKSQQLDEKQQQLNNGEBSMOKKINEIENL 1163
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      250 TNDRLKD--MEHSQTLKNITLLOGARK-----SLT--GKWTNDGSSNMITIGAUNS 297
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db      1164 KNEELKNKELTLEHNETER---LELAQKLNENYEEVKSITERYVLKELQKSPETERDHL 1219
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      298 RGEFTGYTITAVTATSNSEIKES-----PLHGTONTINKRQPTFGFTV----- 340
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db      1220 RG-----YIRIEATGQTKELKIAHILHKEHGETIDELARSRSEKTAQIINTQDLEKS 1274
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      341 NMKPSSESTTVFTGQCFIDRNGKEVLTAKMTMLLRSSVNDI 378
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db      1275 HTKLOEBELPYLHBOELLPNVKEVSET---QETMNEI 1308
      ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 10
US-11-124-368A-215
/ Sequence 215, Application US/11124368A
/ Publication No. US20050287559A1
/ GENERAL INFORMATION:
/ APPLICANT: Michele Cargill
/ APPLICANT: James J. Devlin
/ APPLICANT: May Luke
/ TITLE OF INVENTION: Genetic Polymorphisms Associated with
/ TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
/ FILE REFERENCE: C1001524
/ CURRENT APPLICATION NUMBER: US/11/124,368A
/ CURRENT FILING DATE: 2005-05-09
/ PRIOR APPLICATION NUMBER: US 60/568,845
/ PRIOR FILING DATE: 2004-05-07
/ PRIOR APPLICATION NUMBER: US 60/625,936
/ PRIOR FILING DATE: 2004-11-09
/ NUMBER OF SEQ ID NOS: 2112
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 215
/ LENGTH: 2668
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-11-124-368A-215

```

Query Match	6.1%;	Score 125.5;	DB 7;	Length 2668;
Best Local Similarity	20.1%;	Pred. No. 0.87;		
Matches	92;	Conservative	90;	Mismatches 157;
				Indels 119;
				Gaps 20

```

QY 3 QWDPFPOQOETDCTSYKEDASVALLPBPHKNGPTLOERKSKVKTALITLYLVFV 62
Db 888 EMEQKEDLERDSDTLQVEKFKLITFEKLOQTLBEVKYLTQEKODLKQLOESL----- 941
QY 63 VLVPITIGVAAQLLKWETKNCCTVGSVANADISPSEBKGNGSEDEMRPREAV--MERMSN 119
Db 942 -----QIRBDLKSDIHDVTVMNNID-TOEOLRNALLESJKOHOETINTLKSISE 989
QY 120 MESRIQVLSNDENAL-----LDKKNQNFSTITPOHFNVDLPOLNSILS 163
Db 990 EVSRRILHMEENTGETKCBFOQKRVGIDKQDLEKKNQO-TLTVADVKDNEIIEORRKFIS 1047
QY 164 SIOEHENITIGISKSLVG---INTVLVDQFSIE-TLNG---RVOENAEKQOEE- 210
Db 1048 LIQK-KNELQOMLSVIAEKQOLKT---DLKENIEMTIENTQEBRLLLDELKQOEIVAQ 1103
QY 211 -----MRKLEERINASAEISLDEKQVYLBOEILKGEKMLN-----NI 249
Db 1104 EKNAHAIKKEGELSTCRPLAEVEBKLTAEKSSQOLOEKQOQLNVBENSEMOKKINEINYL 1164
QY 250 TNDRLXND--WEHSQTLKNITLLQGARKC-----SLT--GKWTYDLGSNMTIGAVNS 297

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Db 1164 KNEKNEKLEHETER-----LELAQLENEVEKSIITERKYLKELQSFETERHHL 1219
 Qy 298 RGEFTGYITAVTATSNIEKES-----PLHGTONINKRTOPTGFTV----- 340
 Db 1220 RG-----YIREIATGLOTTKEKIAHILKHEOTIDELRSVSEKTAQIINTDLEKS 1274
 Qy 341 NKPSESTTVPTGCFIDNGKEVAKTMMILRSSVNDI 378
 Db 1275 HTKLOEIPVLHHEOELLPNVAVSET-----OETMNEL 1308

RESULT 11

US-10-793-626-2964
 ; Sequence 2964, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PUS480US
 ; CURRENT APPLICATION NUMBER: US/10/793,626
 ; PRIOR FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 2964
 ; LENGTH: 5024
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: amino acid sequence
 ; NAME/KEY: MOD RES
 ; LOCATION: (5024)
 ; OTHER INFORMATION: variable amino acid
 US-10-793-626-2964

Query Match 5.9%; Score 122.5; DB 6; Length 5024;
 Best Local Similarity 21.5%; Pred. No. 3.3;
 Matches 90; Conservative 64; Mismatches 153; Indels 111; Gaps 17;

Qy 73 AOLKMERKNCVGSVNDISPSPEGKSGSEDEMRFRFAV-----MERMSMESRIQYL 127
 Db 324 AKLYK--AKEDAVASIN-NLS-----GLTNEQKTKENQAVNGSOTRDVAVVLRDSKAL 374
 Qy 128 SDNEANLLDAKNFQNFISITTDQRFNDVLFOQLNSLSIOEHENII-----GDISKSLVG- 181
 Db 375 DOSMOTLADVNVQNVHISTSYNPFEDSTQKTYDNALDNGSTYITGCHNSLANKSTIDQ 434
 Qy 182 ----LNTTVLDI-----QFSIE--TLNG-----RVQ-- 202
 Db 435 TISQINTANLDHGAELQDRDKGTANOIIGQLGYLNDPQSAEBSLVNGSNTRSEVEHL 494
 Qy 203 -----NAFKQSEMRKLEERIVYASAEIKSLDEKQVYLBEGITGEMKLNININDRL 255
 Db 495 NEAKSLNNAKQGLRDVAKETVNGKSSDYINDSTHORGVDQALQEAENIINEIGNP-TL 553
 Qy 256 KDMESQTLKNIT-----LLOGAKKCSLT-----GKMTNDLGSNMTI 292
 Db 554 NKSEIEQKLOUTDQNALQSHLBEAKNNAITEINKULTALNDARQALINVAQOQTI 613
 Qy 293 GAVNSRGEFTGYITAVTATSNIEI-KESPLHGTONINKRTOPTGFTVNMKPSSESTTVF 351
 Db 614 PAVNQOULTDREINFMQALRDVKVQGNVHQQSNVFNEDQF-----KHNYDNSVQ 665
 Qy 352 TGQCCIDR-----NGKEY-----LKTMMILRSSVNDIGDMWKATRVGINIFTLRT 397
 Db 666 AGQCTIIDKQDPINMKNIEQAINQIINTTQALSGENKLTHTQSESTNRQIEGLSLINT 723

RESULT 12

US-10-793-626-1660
 ; Sequence 1660, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PUS480US
 ; CURRENT APPLICATION NUMBER: US/10/793,626
 ; PRIOR FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 1660
 ; LENGTH: 885
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: amino acid sequence
 US-10-793-626-1660

Query Match 5.8%; Score 120; DB 6; Length 885;
 Best Local Similarity 23.4%; Pred. No. 0.49;
 Matches 45; Conservative 41; Mismatches 72; Indels 34; Gaps 7;

Qy 97 ECKNGSEDEMRFRFAVNMERSMESRIQYL-----SDNEANLLDAKNFQNFISITTDQRFN 152
 Db 108 BRKKQSESTNARYE-----BELDNLESQIDISINERAKQNEKLAELKKNQ-----KQLN 156
 Qy 153 DVLFOQLNSLT-SSIOEHENIIIGDISKSLVGLNTTVLDLOFSIETLNGRVOEN----- 203
 Db 157 KEVQELBSLTVISDQHQHEKLEIKNSYVTLMSBQSDVANDIRFLEHTINEBAKKSRLD 216
 Qy 204 ----AFKQ-----QEMKRLERIVYASAEIKSLDEKQVYLBEGITGEMKLNININDRL 254
 Db 217 SRLVAFNQLKDIOQNTQTOKEQYSSKSMKEVQNIQLEQOULTDSKRLSEYENKL- 275
 Qy 255 LKDMESQTLKN 266
 Db 276 YQAVRYNEKLS 287

RESULT 13

US-11-152-697-2
 ; Sequence 2, Application US/11152697
 ; Publication No. US20060003367A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL HUMAN KUPFER CELL RECEPTOR
 ; FILE REFERENCE: D0242 NP
 ; CURRENT APPLICATION NUMBER: US/11/152,697
 ; PRIOR FILING DATE: 2005-06-14
 ; PRIOR APPLICATION NUMBER: 60/580,006
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: Patent In version 3.2
 ; SEQ ID NO 2
 ; LENGTH: 492
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-152-697-2

Query Match 5.6%; Score 115.5; DB 7; Length 492;
 Best Local Similarity 20.9%; Pred. No. 0.47;
 Matches 77; Conservative 53; Mismatches 136; Indels 103; Gaps 14;

Qy 70 IYAADLKRETKNCVGSVNDISPSPEGKSGSEDEMRFRFAVNMERSMESRIQYLSLD 129
 Db 57 VVEIGMLK-----CRVDVNSQLQVLDGHLGNTNAD-IQWVKGVLKDATTLSLQOTMLRS 110
 Qy 130 NEANLLDAKNFQNFISITTDQRFNDVL-FQ-LNSLSLSIOEHENIIIGDISKSLVGLNTTVL 187

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QY      111 S-----LEGTNAEIQRLKEDLEKADALTFQTLNFKSLSENTSEIHLVLSRGLNANSRISQ 166
DB      188 DLOPSIETLNGRVQ-----ENAFKQ-----QEEPRK 213
QY      167 MLNALSLETANTQAQLANSSSLKNAABEIVYLRGHLDSVNDLRTQNOVLNLSLEGANAIEIQ 226
DB      214 LEEBRY-----NASAEIKSL-----DEKQVYLE--- 236
QY      227 LKENQNTNALSQTOAFIKSFDTSAEIQFLRGLERAGDEIHVLRDLKMYTAQOK 286
DB      237 -----QEIKEKMLNITNDLRKDMWHSQTLKNI-TLLOGARKCSLTGKMT 283
QY      287 ANGRLOQDTDTQIQVFKESEMNVTNLAAQIQVLNGHMKASREIQTLKQGMKASALTSQT 346
DB      284 NDIGSNMTIGAV---NSRGEFTGYITAVTATSNKESPLHG--TQNTINKRTPPTGPF 338
QY      347 QMLDSNLQKASAEIQRRLGDLNLTALTWETIQEQSRKLTILHVITTSQEOQLQRTQSOLLO 406
DB      339 TV--NMKFS 345
QY      407 MVLOGMKFN 415
DB

```

```

RESULT 14
US-11-152-697-5
; Sequence 5, Application US/11152697
; Publication No. US20060003367A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL HUMAN KUPFERER CELL RECEPTOR
; FILE REFERENCE: D0242 NP
; CURRENT APPLICATION NUMBER: US/11/152,697
; PRIOR FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/580,006
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-152-697-5

```

```

Query Match      5.6%; Score 115.5; DB 7; Length 539;
Best Local Similarity 20.9%; Pred. No. 0.53; Indels 103; Gaps 14;
Matches 77; Conservative 53; Mismatches 136;

```

```

QY      70 IVAQLLKWETKCTVGSVNADISPSGKNGSEDEMRFEAVVMERSMNSRISQYLSQ 129
DB      118 VVEIQMLK-----CRVDVNSQLQVLGDLHNTAND-IQWVGVLKADATTLISLQMLRS 171
QY      130 NEANLLDANKFONFSITTDQRFNDVL-FQ-INSLLSSIQEHENITIGDISKVLGLNTTVL 187
DB      172 S-----LEGTNAEIQRLKEDLEKADALTFQTLNFKSLSENTSEIHLVLSRGLNANSRISQ 227
QY      188 DLOPSIETLNGRVQ-----ENAFKQ-----QEEPRK 213
DB      228 MLNALSLETANTQAQLANSSSLKNAABEIVYLRGHLDSVNDLRTQNOVLNLSLEGANAIEIQ 287
QY      214 LEEBRY-----NASAEIKSL-----DEKQVYLE--- 236
DB      288 LKENQNTNALSQTOAFIKSFDTSAEIQFLRGLERAGDEIHVLRDLKMYTAQOK 347
QY      237 -----QEIKEKMLNITNDLRKDMWHSQTLKNI-TLLOGARKCSLTGKMT 283
DB      348 ANGRLOQDTDTQIQVFKESEMNVTNLAAQIQVLNGHMKASREIQTLKQGMKASALTSQT 407
QY      284 NDIGSNMTIGAV---NSRGEFTGYITAVTATSNKESPLHG--TQNTINKRTPPTGPF 338
DB      408 QMLDSNLQKASAEIQRRLGDLNLTALTWETIQEQSRKLTILHVITTSQEOQLQRTQSOLLO 467

```

```

QY      339 TV--NMKFS 345
DB      468 MVLOGMKFN 476

```

```

RESULT 15
US-10-793-626-3154
; Sequence 3154, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3154
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3154

```

```

Query Match      5.4%; Score 110.5; DB 6; Length 1095;
Best Local Similarity 20.8%; Pred. No. 3.1; Indels 87; Gaps 14;
Matches 71; Conservative 59; Mismatches 125;

```

```

QY      111 EAVVMSMNSRISQYLSDNENANLLDANKFONFSIT-----TDQRFNDVLPQANSL 162
DB      469 EAVQLKVNDAIHTMLQNKENNSA-LVTAKNQLQAVNDDPLTGTGTQDSINNVAARNBAQ 527
QY      163 SSIQEHENIT--GD-----ISKSLVGLN-----TVVLDLOPSIETLNGRVQ 201
DB      528 SAIRNAEAVINNGDATABAKQISDEKSKVQALAHINDAKQQLADTTLBELQTAIVQQLNRG 587
QY      202 ENAFKQ-----EEMKLERIYNASAEISLDEKQVYLEQEIKEKMLNITNDL-- 253
DB      588 TNKKPRINAYNAKIOSLETQITSADKANANAVIQPIRTVOEVNNAQLQVNLQQLTE 647
QY      254 ---RLKDMWHSQTLK-----NITLQARKCSLTGKMTNDLS 288
DB      648 AINQLOPLSNNDALKARLNLENKINQVOTDGMTQOSIEAVQNAKRYA-----QNE--S 700
QY      289 NMTIGAVNSRGEFTGYITAVTATSNKESPLHGTONTKRTPPTGFTVNMKFSRST 348
DB      701 NTALALINN-GDADEQQLTTEBDRVN-----QOTTN-LTQALINGLTVNKEPLE-- 746
QY      349 TVFTGCCPIDNGKEVLTMTMLRSSVNDIGDDMKATRVGIN 390
DB      747 ---TAKTALQNNIDQVPSDGMTQOSVANYNQKLQIANKEIN 785

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```

Search completed: February 16, 2006, 17:09:55
Job time : 20 secs

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